V

Seq. Listing

Please type a plus (+) inside this box → ⊞

PTO/SB/29 (12/97)
Approved for use through 09/30/00. OMB 0651-0032
Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

JC61 U.S. PTO 01/25/99

UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	8907-0078-999
Total Pages	
First Named Inventor or Application Identifier	Thomas Quertermous et al.
Express Mail Label No.	EL 236 251 638 US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: **Assistant Commissioner for Patents**
Box Patent Application
Washington, DC 20231

1. ☒ Fee Transmittal Form
   Submit an original, and a duplicate for fee processing)
2. ☒ Specification Total Sheets[99]
   (preferred arrangement set forth below)
   - -Descriptive title of the Invention
   - -Cross Reference to Related Applications
   - -Statement Regarding Fed sponsored R&D
   - -Reference to Microfiche Appendix
   - -Background of the Invention
   - -Brief Summary of the Invention
   - -Brief Description of the Drawings *(if filed)*
   - -Detailed Description of the Invention (including drawings, *if filed*)
   - -Claim(s)
   - -Abstract of the Disclosure
3. Drawing(s) *(35 USC 113)* Total Sheets[32]
4. Oath or Declaration [2]
   - a. ☐ Newly executed (original or copy)
   - b. ☒ Copy from a prior application (37 CFR 1.63(d)) *(for continuation/divisional with Box 17 completed)* ***[Note Box 5 below]***
   - i. ☐ DELETION OF INVENTORS(S)
     Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33 (b).
5. ☒ Incorporation By Reference *(useable if Box 4b is checked)*
   The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
6. ☐ Microfiche Computer Program *(Appendix)*
7. ☒ Nucleotide and/or Amino Acid Sequence Submission *(if applicable, all necessary)*
   - a. ☐ Computer Readable Copy
   - b. ☒ Paper Copy (identical to computer copy)
   - c. ☐ Statement verifying identity of above copies

JC542 U.S. PTO 09/237781 01/25/99

ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & document(s))
9. ☐ 37 CFR 3.73(b) Statement *(when there is an assignee)* ☐ Power of Attorney
10. ☐ English Translation Document *(if applicable)*
11. Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
12. ☒ Preliminary Amendment
13. ☒ Return Receipt Postcard (MPEP 503) *(Should be specifically itemized)*
14. ☐ Small Entity Statement(s) ☒ Statement filed in prior application, Status still proper and desired
15. ☐ Certified Copy of Priority Document(s) *(if foreign priority is claimed)*
16. ☐ Other:

17. If a CONTINUING APPLICATION, *check appropriate box and supply the requisite information:*
☐ Continuation ☒Divisional ☐Continuation-in-part (CIP) of prior application No: 08/659,235 filed 06/05/96.

18. CORRESPONDENCE ADDRESS

☒ Customer Number or Bar Code Label: 20583 *(Insert Customer No. or Attach bar code label here)* or ☐ Correspondence address below

NAME					
ADDRESS					
CITY		*STATE*		*ZIP CODE*	
COUNTRY		*TELEPHONE*		*FAX*	

Burden Hour Statement: This form is estimated to take 0.2 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231.

01/25/99 jc611 U.S. PTO

PENNIE & EDMONDS LLP DOCKET NO. 8907-0078-999 Express Mail No. EL 236 251 638 US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Anticipated Classification of this application:

Prior application: Examiner KAUFMAN, C.

Art Unit 1646

Assistant Commissioner for Patents
Box PATENT APPLICATION
Washington, D.C. 20231

Sir:

This is a request for filing a ☐continuation ☒divisional application under 37 CFR § 1.53(b), of pending prior application no. 08/659,235 filed on June 5, 1996.

of Thomas Quertermous, Brigid Hogan, H. Ralph Snodgrass, Thomas J. Zupancic
(inventor(s) currently of record in prior application)

for ANTIBODIES BINDING TO POLYPEPTIDES ENCODED BY DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1.
(title of invention)

1. ☒ The filing fee is calculated below:

PATENT APPLICATION FEE VALUE

TYPE	NO. FILED	LESS	EXTRA	EXTRA RATE	FEE
Total Claims	32	-20	12	$9.00 each	108.00
Independent	4	-3	1	$39.00 each	39.00
				Basic Fee	760.00
				Multiple Dependency Fee If Applicable ($270.00)	
				Total	907.00
				50% Reduction for Independent Inventor, Nonprofit Organization or Small Business Concern	- 453.50
				Total Filing Fee	$ 453.50

2. ☒ Please charge the required fee to Pennie & Edmonds LLP Deposit Account No. 16-1150. A copy of this sheet is enclosed.

3. ☐ Amend the specification by inserting the following sentence: --This is a divisional of application no. ________, filed __________.--

4a. ☐ Transfer the drawings from the prior application to this application and abandon the prior application as of the filing date accorded this application. A duplicate copy of this sheet is enclosed for filing in the prior application file.

4b. ☐ New formal drawings are enclosed.

4c. ☒ Informal drawings are enclosed.

5a. ☐ Priority of application no. __________ filed on ________ in _____is claimed under 35 U.S.C. §119.

5b. ☐ The certified copy has been filed in prior application no. ________, filed ____________.

6. ☒ The prior application is assigned of record to Progenitor, Inc. and Vanderbilt University.

7a. ☒ The Power of Attorney appears in the original papers in the prior application no. 08/659,235, filed June 5, 1996. (Copies are attached.)

7b. ☐ Since the Power of Attorney does not appear in the original papers, a copy of the Power in prior application no. ________, filed _____ is enclosed.

8. ☒ This application contains nucleic acid and/or amino acid sequences required to be disclosed in a Sequence Listing under 37 CFR §§1.821-1.825. It is requested that the Sequence Listing in computer readable form from prior application no. 08/659,235, filed on June 5, 1996, be made a part of the present application as provided for by 37 C.F.R. §1.821(e). The sequences disclosed therein are the same as the sequences disclosed in this application. A copy of the paper Sequence Listing from application no. 08/659,235 is enclosed.

9. ☒ The undersigned states, under 37 C.F.R. §1.821(f), that the content of the enclosed paper Sequence Listing from application no. 08/659,235 is the same as the content of the computer readable form submitted in application no. 08/659,235.

10. ☒ Please cancel Claims 1-20 and 28-32.

11. ☒ Preliminary Amendment and new claims are attached.

Respectfully submitted,

January 25, 1999
(date)

Brian M. Poissant / by Victor N. Lee Reg No. 35,750

Brian M. Poissant

28,462
(Reg No.)

PENNIE & EDMONDS LLP
1155 Avenue of the Americas
New York, NY 10036
Tel. No. (212) 790-9090

Jc617 U.S. PTO
01/25/99

Express Mail No. EL 236 251 638 US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Quertermous et al.

Serial No.: To Be Assigned

Group Art Unit: To Be Assigned

Filed: Concurrently with Rule 53(b) Divisional Application of Serial No. 08/659,235

Examiner: To Be Assigned

Attorney Docket No.: 8907-078-999

For: DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Prior to the examination of the above-identified application, please consider the following amendments and remarks.

IN THE TITLE

At page (i), line 1, and at page 1, line 3, please delete the title and insert the following in its place:

--ANTIBODIES BINDING TO POLYPEPTIDES ENCODED BY DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1--.

IN THE SPECIFICATION

At page ii, lines 27-31, please delete the paragraph on priority information and insert the following in its place:

--This is a divisional application of United States Patent Application Serial No. 08/659,235, filed June 5, 1996 (allowed), which is a continuation-in-part of United States Patent Application Serial No. 08/480,229, filed June 7, 1995 (allowed), each of which is incorporated herein in its entirety.--

IN THE CLAIMS

Please cancel Claims 21-27 and 33 without prejudice.

Please add the following new claims:

--34. (New) An antibody which binds to a polypeptide, said polypeptide comprising the amino acid sequence as shown in SEQ ID NO:10, or a fragment of the antibody that binds said polypeptide.

35. (New) The antibody of Claim 34 which specifically binds to a structurally unique epitope in the polypeptide.

36. (New) The antibody of Claim 34 which is a Fab, $F(ab')_2$, single chain or chimeric.

37. (New) The antibody of Claim 34 which is a polyclonal antibody.

38. (New) The antibody of Claim 34 which is a monoclonal antibody.

39. (New) The antibody of Claim 34 which competitively inhibits the binding of said polypeptide to alpha V beta 3.

40. (New) A method of detecting a Del-1-expressing cell in a cell mixture, comprising incubating the cell mixture with the antibody of Claim 34; and detecting an antibody-bound cell.

41. (New) The method of Claim 40 in which the antibody is linked to a detectable label.

42. (New) An antibody which binds to a polypeptide, said polypeptide comprising the amino acid sequence as shown in SEQ ID NO:29, or a fragment of the antibody that binds said polypeptide.

43. (New) The antibody of Claim 42 which specifically binds to a structurally unique epitope in the polypeptide.

44. (New) The antibody of Claim 42 which is a Fab, $F(ab')_2$, single chain or chimeric.

45. (New) The antibody of Claim 42 which is a polyclonal antibody.

46. (New) The antibody of Claim 42 which is a monoclonal antibody.

47. (New) The antibody of Claim 42 which competitively inhibits the binding of said polypeptide to alpha V beta 3.

48. (New) A method of detecting a Del-1-expressing cell in a cell mixture, comprising incubating the cell mixture with the antibody of Claim 42; and detecting an antibody-bound cell.

49. (New) The method of Claim 48 in which the antibody is linked to a detectable label.

50. (New) An antibody which binds to a polypeptide, said polypeptide comprising the amino acid sequence as shown in SEQ ID NO:14 from residues #33 through #513, or a fragment of the antibody that binds said polypeptide.

51. (New) The antibody of Claim 50 which specifically binds to a structurally unique epitope in the polypeptide.

52. (New) The antibody of Claim 50 which is a Fab, $F(ab')_2$, single chain or chimeric.

53. (New) The antibody of Claim 50 which is a polyclonal antibody.

54. (New) The antibody of Claim 50 which is a monoclonal antibody.

55. (New) The antibody of Claim 50 which competitively inhibits the binding of said polypeptide to alpha V beta 3.

56. (New) A method of detecting a Del-1-expressing cell in a cell mixture, comprising incubating the cell mixture with the antibody of Claim 50; and detecting an antibody-bound cell.

57. (New) The method of Claim 56 in which the antibody is linked to a detectable label.

58. (New) An antibody which binds to a polypeptide, said polypeptide comprising the amino acid sequence as shown in SEQ ID NO:14 from residues #33 through #513 with the exception that the amino acid sequence from residues #98 through #107 is removed.

59. (New) The antibody of Claim 58 which specifically binds to a structurally unique epitope in the polypeptide.

60. (New) The antibody of Claim 58 which is a Fab, F(ab')2, single chain or chimeric.

61. (New) The antibody of Claim 58 which is a polyclonal antibody.

62. (New) The antibody of Claim 58 which is a monoclonal antibody.

63. (New) The antibody of Claim 58 which competitively inhibits the binding of said polypeptide to alpha V beta 3.

64. (New) A method of detecting a Del-1-expressing cell in a cell mixture, comprising incubating the cell mixture with the antibody of Claim 58; and detecting an antibody-bound cell.

65. (New) The method of Claim 64 in which the antibody is linked to a detectable label.--

REMARKS

This Preliminary Amendment is being submitted concurrently with Applicants' Request for Filing a Divisional under 37 C.F.R. § 1.53(b) of parent Application Serial No. 08/659,235, filed June 5, 1996. In this Amendment, Claims 21-27 and 33 have been cancelled, and replaced by new Claims 34-65. Claims 21-27 and 33 were encompassed in

Group IV in a Restriction Requirement dated February 11, 1997 in connection with the parent application. The new claims are supported by the specification at page 36, line 28 to page 39, line 2. More specifically, the polypeptide recited in Claim 34 is described in Figure 3A-3E. The polypeptide recited in Claim 42 is described in Figure 12A-12E. The polypeptide recited in Claim 50 is described in Figure 4A-4C. The polypeptide recited in Claim 58 is described at page 49, lines 23-27 and in Figure 11. Claims 36-38, 44-46, 52-54 and 60-62 are described at page 36, lines 30-33, and page 38, lines 1-11 and lines 28-37. Claims 39, 47, 55 and 63 are described at page 25, lines 32-34. Claims 40, 48, 56 and 64 are described at page 25, line 36 to page 26, line 2. No new matter has been introduced by the new claims.

The title of the application has been amended to reflect the presently claimed invention. The specification has been amended to insert up-dated priority information. The amendments do not introduce new matter.

Applicants respectfully request that this Amendment be made of record in the file history of the instant application.

Respectfully submitted,

Dated: January 25, 1999

Brian M. Poissant / by Victor ... Reg. No. 35,750
Brian M. Poissant ~~28,462~~ (Reg. No.)

PENNIE & EDMONDS LLP
1155 Avenue of the Americas
New York, New York 10036-2711
(212) 790-9090

Enclosure

CA1 - 207783.1

EXPRESS MAIL No. TB665381288US

jc617 U.S. PTO
01/25/99

DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

TABLE OF CONTENTS

The present application is a continuation-in-part of co-pending United States Patent Application Serial No. 08/480,229, filed June 7, 1995, which is incorporated by reference herein in its entirety.

DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

This invention was made, in part, with government support under HD 25580 awarded by the National Institutes of Health. The government may have certain rights in the invention.

1. INTRODUCTION

The present invention relates to a member of a novel gene family referred to as developmentally-regulated endothelial cell locus-1 (*del-1*). In particular, the invention relates to *del-1* nucleotide sequences, Del-1 amino acid sequences, methods of expressing a functional gene product, antibodies specific for the gene product, and methods of using the gene and gene product. Since *del-1* is expressed in endothelial cells and certain cancer cells, it may be useful as an endothelial cell and tumor marker. In addition, the ability of Del-1 protein to inhibit vascular formation provides for its use as an anti-angiogenic agent.

2. BACKGROUND OF THE INVENTION

2.1. ENDOTHELIAL CELL BIOLOGY AND BLOOD VESSEL DEVELOPMENT

The endothelium occupies a pivotal position at the interface between the circulating humoral and cellular elements of the blood, and the solid tissues which constitute the various organs. In this unique position, endothelial cells regulate a large number of critical processes. Such processes include leukocyte adherence and transit through the blood vessel wall, local control of blood vessel tone, modulation of the immune response, the balance between thrombosis and thrombolysis, and new blood vessel development (Bevilacqua et al., 1993, *J. Clin. Invest* 91:379-387; Folkman et al., 1987, *Science* 235:442-447; Folkman et al., 1992, J. Biol. Chem. 267:10931-10934; Gimbrone, 1986, Churchill Livingstone, London; Issekutz, 1992, *Curr. Opin. Immunol.*

4:287-293; Janssens et al., 1992, *J. Biol. Chem.* 267:14519-14522; Lamas et al., 1992, *Proc. Natl. Acad. Sci. U.S.A.* 89:6348-6352; Luscher et al., 1992, *Hypertension* 19:117-130; Williams et al., 1992, *Am. Rev. Respir. Dis.* 146:S45-S50; Yanagisawa, et al., 1988, *Nature* 332:411-415).

Endothelial cell dysfunction has been postulated as a central feature of vascular diseases such as hypertension and atherosclerosis. In this context, the ability of the endothelium to synthesize smooth muscle cell mitogens and factors which control smooth muscle contraction has received much attention (Janssens et al., 1992, *J. Biol. Chem.* 267:14519-14522; Lamas et al., 1992, *Proc. Natl. Acad. Sci. U.S.A.* 89:6348-6352; Luscher et al., 1992, *Hypertension* 19:117-130; Raines et al., 1993, *Br. Heart J.* 69:S30-S37; Yanagisawa et al., 1988, *Nature* 332:411-415). The endothelial cell has also become the focus of attention in the study of diseases which are not primarily vascular in nature. Diverse disease processes such as adult respiratory distress syndrome, septic shock, solid tumor formation, tumor cell metastasis, rheumatoid arthritis, and transplant rejection are now understood to be related to normal or aberrant function of the endothelial cell. A rapidly increasing number of pharmacologic agents are being developed whose primary therapeutic action will be to alter endothelial cell function. In addition, recent attention on gene therapy has focused on the endothelial cell (Nabel et al., 1991, *J. Am. Coll. Cardiol.* 17:189B-194B). Transfer of genes into the endothelial cell may afford a therapeutic strategy for vascular disease, or the endothelium may serve simply as a convenient cellular factory for a missing blood borne factor. Hence, information regarding fundamental processes in the endothelial cell will aid the understanding of disease processes and allow more effective therapeutic strategies.

Studies from a number of laboratories have characterized the ability of the endothelial cell to dramatically alter basic activities in response to cytokines such as tumor 3necrosis factor (TNF)-alpha. TNF-alpha stimulation induces

significant alterations in the production of vasoactive compounds such as nitric oxide and endothelin, increases surface stickiness toward various types of leukocytes, and modulates the expression of both pro- and anti-coagulant factors (Cotran et al., 1990, *J. Am. Soc. Nephrol.* 1:225-235; Mantovani et al., 1992, *FASEB J.* 6:2591-2599). In turn, endothelial cells have been shown to be an important source for the production of cytokines and hormones, including interleukin 1, 6 and 8 (Gimbrone et al., 1989, *Science* 246:1601-1603; Locksley et al. 1987, *J. Immunol.* 139:1891-1895; Loppnow et al., 1989, *Lymphokine. Res.* 8:293-299; Warner et al., 1987, *J. Immunol.* 139:1911-1917).

The ability of endothelial cells to produce granulocyte, granulocyte-macrophage, and macrophage colony stimulating factors has led to speculation that endothelial cells are an important facet of hematopoietic development (Broudy et al., 1987, *J. Immunol.* 139:464-468; Seelentag et al., 1987, *EMBO J.* 6:2261-2265). Early studies have provided the foundation for the cloning of a large number of "endothelial cell-specific" genes. Some of these include ICAM-1, ICAM-2, VCAM-1, ELAM-1, endothelin-1, constitutive endothelial cell nitric oxide synthetase, thrombomodulin, and the thrombin receptor (Bevilacqua et al., 1989, *Science* 243:1160-1165; Jackman et al., 1986, *Proc. Natl. Acad. Sci. U.S.A.* 83:8834-8838; Janssens et al., 1992, *J. Biol. Chem.* 267:14519-14522; Lamas et al., 1992, *Proc. Natl. Acad. Sci. U.S.A.* 89:6348-6352; Osborn et al., 1989, *Cell* 59:1203-1211; Staunton et al., 1989, *Nature* 339:61-64; Staunton et al., 1988, *Cell* 52:925-933; Vu et al, 1991, *Cell* 64:1057-1068; Yanagisawa et al., 1988, *Nature* 332:411-415).

All blood vessels begin their existence as a capillary, composed of only endothelial cells. Much of the molecular research investigating the role of endothelial cells in blood vessel development has focused on this process in the adult organism, in association with pathological conditions. In these situations, new blood vessels are formed by budding and branching of existing vessels. This process, which depends

on endothelial cell division, has been termed angiogenesis. Research on this process has focused primarily on small proteins which are growth factors for endothelial cells (Folkman et al., 1987, *Science* 235:442-447; Folkman et al., 1992, *J. Biol. Chem.* 267:10931-10934). Sensitive bioassays for angiogenesis have allowed the characterization of a number of angiogenic factors, from both diseased and normal tissues. Members of the fibroblast growth factor (FGF) family, platelet-derived endothelial cell growth factor, and vascular endothelial cell growth factor (vascular permeability factor), are a few of the angiogenic factors which have been characterized (Folkman et al., 1987, *Science* 235:442-447; Folkman et al., 1992, *J. Biol. Chem.* 267:10931-10934; Ishikawa et al., 1989, *Nature* 338:557-562; Keck et al., 1989, *Science* 246:1309-1312; Leung et al., 1989, *Science* 246:1306-1309).

Such information has provided some insight into the study of blood vessel development in the embryo. Studies linking vascular development to an angiogenic factor have resulted in the work with vascular endothelial cell growth factor (VEGF). VEGF expression has been correlated in a temporal and spatial fashion with blood vessel development in the embryo (Breier et al., 1992, *Development* 114:521-532). A high affinity VEGF receptor, *flk-1*, has been shown to be expressed on the earliest endothelial cells in a parallel fashion (Millauer et al., 1993, *Cell* 72:835-846).

Blood vessels form by a combination of two primary processes. Some blood vessel growth depends on angiogenesis, in a process very similar to that associated with pathological conditions in the adult. For instance, the central nervous system depends solely on angiogenesis for development of its vascular supply (Noden, 1989, *Am. Rev. Respir. Dis.* 140:1097-1103; Risau et al., 1988, *EMBO J.* 7:959-962). A second process, vasculogenesis, depends on the incorporation of migratory individual endothelial cells (angioblasts) into the developing blood vessel. These angioblasts appear to be components of almost all mesoderm,

and are able to migrate in an invasive fashion throughout the embryo (Coffin et al., 1991, *Anat. Rec.* 231:383-395; Noden, 1989, *Am. Rev. Respir. Dis.* 140:1097-1103; Noden, 1991, *Development* 111:867-876). The precise origin of this cell, and the characteristics of its differentiation have not been defined.

Understanding of the molecular basis of endothelial cell differentiation in blood vessel development may allow manipulation of blood vessel growth for therapeutic benefit. The ability to suppress blood vessel growth may also provide therapeutic strategies for diseases such as solid tumors and diabetic retinopathy. On the other hand, diseases such as coronary artery disease may be treated through pharmacologic induction of directed blood vessel growth, through increasing collateral circulation in the coronary vascular bed. Both vascular diseases such as atherosclerosis and hypertension and nonvascular diseases which depend on the endothelial cell will benefit from a better understanding of endothelial cells.

2.2. EPIDERMAL GROWTH FACTOR-LIKE DOMAIN

Epidermal growth factor (EGF) stimulates growth of a variety of cell types. EGF-like domains have been found in a large number of extracellular and membrane bound proteins (Anderson, 1990, *Experientia* 46(1):2; and Doolittle, 1985, *TIBS*, June:233). These proteins include molecules that function as soluble secreted proteins, growth factors, transmembrane signal and receptor molecules, and components of the extracellular matrix (Lawler and Hynes, 1986, *J. Cell. Biol.* 103:1635; Durkin et al., 1988, *J. Cell Biol.* 107:2749; Wu et al., 1990, *Gene* 86:275; Bisgrove and Raff, 1993, *Develop. Biol.* 157:526;).

In many cases, multiple tandem repeats of a characteristic 40 amino acid long, 6 cysteine-containing sequence are observed (Anderson, 1990, *Experientia* 46(1):2). EGF-like domains are homologous to the peptide growth factor EGF which consists of a single copy of the standard EGF

domain. These domains have been highly conserved in evolution, being found in species as diverse as nematodes, Drosophila, sea urchins, and vertebrates.

The EGF molecule and the closely related transforming growth factor (TGF) alpha induce cell proliferation by binding to a tyrosine kinase receptor. It has been suggested that other EGF-like domains also function as ligands for receptor molecules (Engel, 1989, *FEBS Lett.* 251:1-7). Fundamentally, EGF repeats are protein structures that participate in specific protein-protein binding interactions.

The Drosophila Notch protein, the Nematode lin-12 and glp-1 proteins, and the closely related vertebrate homologs, Motch (mouse Notch), Xotch (Xenopus Notch), rat Notch, and TAN 1 (human Notch) are membrane bound receptor molecules that control the specification of cell fate for a variety of cell types early in embryogenesis (Rebay et al., 1991, *Cell* 67:687; Hutter and Schnabel, 1994, *Development* 120:2051; Del Amo et al 1992, *Development* 115:737; Reaume et al. 1992 *Develop. Biol.* 154:377; and Ellisen et al., 1991, *Cell* 66:649). Specific EGF-like repeats in the Notch receptors are binding sites that attach to protein ligands leading to signal transduction (Rebay et al., 1991 *Cell* 67:687; Couso and Arias, 1994, *Cell* 79:259; Fortini and Artavanis-Tsakonas, 1994, *Cell* 79:273; Henderson et al., 1994, *Development* 120:2913). Extracellular matrix proteins such as thrombospondin, entactin, tenascin and laminin play key roles in morphogenesis by providing the physical scaffold to which cells attach to form and maintain tissue morphologies (Frazier, 1987, *J. Cell. Biol.* 105:625; Taraboletti et al., 1990, *J. Cell. Biol.* 111:765; Ekblom et al., 1994, *Development* 120:2003).

2.3. DISCOIDIN I/FACTOR VIII-LIKE DOMAINS

A homologous domain structure has been discovered in coagulation factors VIII and V (Kane and Davie, 1986, *Proc. Natl. Acad. Sci. U.S.A.* 83:6800). This domain is related to a more ancient structure first observed in the discoidin I

protein produced by the cellular slime mold *Dictyostelium discoideum*. Discoidin I is a carbohydrate binding lectin secreted by Dictyostelium cells during the process of cellular aggregation and is involved in cell-substratum attachment and ordered cell migration (Springer et al., 1984, *Cell* 39:557).

Discoidin I/factor VIII-like domains have also been observed in a number of other proteins. For example, milk fat globule protein (BA46), milk fat globule membrane protein (MFG-E8), breast cell carcinoma discoidin domain receptor (DDR), and the Xenopus neuronal recognition molecule (A5) (Stubbs et al., 1990, *Proc. Natl. Acad. Sci. U.S.A.* 87:8417; Larocca et al., 1991, *Cancer Res.* 51:4994; Johnson et al., 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5677). The discoidin I/factor VIII-like domains of the vertebrate proteins are all distantly related to the Dictyostelium sequence but more closely related to each other.

Discoidin I/factor VIII-like domains are rich in positively charged basic amino acids and are believed to bind to negatively charged substrates such as anionic phospholipids or proteoglycans. Both of the milk fat globule proteins have been shown to associate closely with cell membranes and the coagulation factors VIII and V interact with specific platelet membrane proteins (Stubbs et al., 1990 *Proc. Nat. Acad. Sci. U.S.A.* 87:8417; Larocca et al., 1991, *Cancer Res.* 51:4994).

3. SUMMARY OF THE INVENTION

The present invention relates to a novel gene family referred to as *del-1*. In particular, it relates to *del-1* nucleotide sequences, expression vectors containing the sequences, genetically-engineered host cells expressing *del-1*, Del-1 protein, Del-1 mutant polypeptides, methods of expressing *del-1* and methods of using *del-1* and its gene product in various normal and disease conditions such as cancer.

The invention is based, in part, upon Applicants' isolation of a murine DNA clone (SEQ ID NO: 9), *del-1*, and its homologous human counterpart (SEQ ID NO: 11). Structural features of the Del-1 protein are deduced by homology comparisons with sequences in the Genbank and NBRF-PIR databases. The protein is a modular molecule composed of repeats of two different sequence motifs which are present in a number of distinct proteins. The two sequence motifs are known as the EGF-like domain (SEQ ID NO: 26) and the discoidin I/factor VIII-like domain (SEQ ID NOS: 1-8). These domains are defined by characteristic patterns of conserved amino acids distributed throughout the molecule at specific locations. While Del-1 shows certain sequence homology with other proteins, it is unique in both its primary sequence and its overall structure. In all cases in which EGF-like and discoidin I-like domains have been identified, both of these structures are always found in extracellular locations. Variant forms of Del-1 protein exist, and one form is shown herein to be an extracellular matrix protein and is associated with the cell surface. The expression pattern of *del-1* further indicates that it is involved in endothelial cell function. In addition, a number of human tumor cells express *del-1*. Furthermore, host-derived blood vessels that traverse the tumor nodule also express *del-1*. The Del-1 protein inhibits vascular morphogenesis and binds to $\alpha V\beta 3$ as its cellular receptor. Therefore, a wide variety of uses are encompassed by the present invention, including but not limited to, the use of Del-1 as a tumor marker for cancer diagnosis and treatment, the isolation of embryonic endothelial cells, the identification of Del-1 binding partners, and the stimulation or inhibition of endothelial cell growth and blood vessel formation.

4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Genomic organization of 42 kb of the murine *del-1* locus, as characterized by cloning from a λfix library constructed

from the SLM275 transgenic mouse, and a wildtype 129SV λfix library. The dashed line indicates DNA studied to date by zoo blot and exon trapping. The location of the exon identified by exon trapping is shown.

Figure 2. Homology analysis between the deduced amino acid sequence of the putative *del-1* gene (m-del1) (SEQ ID NO: 1) and other proteins with "discoidin-like domains." Identical residues are boxed, conserved residues are shaded (Geneworks, Intelligenetics, Mountain View, CA). m-del-1 sequence (SEQ ID NO: 1) was derived from a trapped exon and mouse embryo cDNAs. Abbreviations:h-MFG, human milk fat globule protein (SEQ ID NO: 2); h-FV, human coagulation factor V (SEQ ID NO: 3); m-FVIII, mouse coagulation factor VIII (SEQ ID NO: 4); X-A5b1 (SEQ ID NO: 5) and X-A5b2 (SEQ ID NO: 6), b1 and b2 domains of Xenopus neuronal antigen A5; dis-I, discoidin I (SEQ ID NO: 7).

Figure 3A-3E. Nucleotide sequence and deduced amino acid sequence of murine *del-1* cDNA (SEQ ID NO: 9).

Figure 4A-4C. Nucleotide sequence and deduced amino acid sequence of human *del-1* cDNA (SEQ ID NO: 11).

Figure 5. Murine *del-1* fragment (SEQ ID NO: 19) used as probe for human *del-1* cloning and Northern blot analysis.

Figure 6. Amino acid sequence comparison between murine (m-del-1) (SEQ ID NO: 10) and human (h-del-1) (SEQ ID NO: 29) Del-1 proteins. The EGF-like and discoidin-like domains are indicated by "egf" and "discoidin," respectively.

Figure 7. The small rectangles labeled "EGF" show the location and relative sizes of the three EGF-like domains of Del-1. These regions of the protein are approximately 40 amino acids long. Each EGF-like domain contains six cysteine residues and additional conserved amino acids, distributed in a pattern which is highly conserved among proteins that contain this common motif. In addition, the amino acid sequence RGD occurs in the center of the second EGF-like repeat. This sequence is found in a variety of extracellular matrix proteins and, in some cases, it is required for binding to integrin proteins. An RGD sequence is present in the same position in the second EGF-like repeat of MFG-E8.
The large rectangles on the right side represent tandem discoidin I/factor VIII-like domains. This protein motif is based on a conserved pattern of amino acids defined by the homology between the *D. discoidium* discoidin I protein and mammalian coagulation factor VIII.

Figure 8. The 54.2% amino acid homology between human Del-1 and MFG-E8 (SEQ ID NO: 21) in the tandem discoidin I/factor VIII domains is shown. These domains are rich in the basic amino acids arginine and lysine. The 5'

domain contains 12 arginines and 12 lysines versus 9 acidic residues, while the 3' domain contains 8 arginines and 10 lysines versus 16 acidic residues. A similar domain in the coagulation factor VIII protein is believed to bind to negatively charged phospholipids on the surface of platelets. The MFG-E8 protein has been found to associate tightly with milk fat globule membranes.

Figure 9. The predicted amino acid sequence at the amino terminus of the human Del-1 protein (SEQ ID NO: 22) shows characteristics common to signal peptides. The putative signal begins with a basic arginine residue and is followed by a stretch of 18 amino acids rich in hydrophobic residues. Signal peptides typically end with a small amino acid such as glycine or alanine. In addition, the Chou and Fasman algorithm predicts that the putative signal sequence is followed by a protein turn structure, a feature commonly found after signal peptides. The Del-1 protein is secreted by expressing cells.

Figure 10. Sequence similarities between the three EGF-like domains of Del-1 (SEQ ID NOS: 23-25) and homology with the consensus EGF-like domain amino acid sequence (SEQ ID NO: 26). Also, the amino acid sequence RGD is in the center of the second EGF-like repeat. This sequence is found in a variety of extracellular matrix proteins and, in some cases is required for binding to integrin proteins. An RGD sequence is present in the

same position in the second EGF-like repeat of MFG-E8.

Figure 11. Human *del-1* splicing variant partial sequence (SEQ ID NO: 27) showing the variation as compared with the major form.

Figure 12A-12E. Murine *del-1* truncated minor nucleotide and deduced amino acid sequences (SEQ ID NO: 28).

Figure 13A-13H. X-gal staining in whole mount and tissue sections of embryos from the SLM275 line. (13A) Embryo at 7.5 days pc (headfold stage) stained as whole mount. X-gal staining is seen in cells of the extraembryonic mesoderm (xm) which will give rise to the yolk sac and associated blood islands. Abbreviations: ng, neural groove. Photographed at 70x. (13B) Section of yolk sac blood islands from 8 day pc embryo stained as a whole mount with membranes intact and subsequently sectioned and counterstained. Clusters of round cells in the blood islands show X-gal staining (arrow), while mature endothelial cells do not stain (open arrowhead). Photographed at 400x. (13C) Embryo at 9.5 days pc. Prominent X-gal staining (blue-green) is seen in the heart and outflow tract (mid-portion of embryo). In addition, the aorta (arrowhead) and intervertebral vessels are stained. Photographed at approximately 30x, darkfield illumination. (13D) Section of 9.5 day embryo showing heart and outflow tract. This section indicates that X-gal staining in the heart and outflow tract is

restricted to the endothelial cells (endocardium). Section was counterstained with hematoxylin and eosin, photographed at 200x. (13E) Embryo at 13.5 days pc, dissected and X-gal stained as a whole mount. At this stage, as confirmed by study of tissue sections, endothelial cells lining the ventricle (v) and large vessels such as the aorta (filled arrowhead) have lost most of their staining. Staining of the endothelial cells of the atrium (a) has diminished but is still apparent in the whole mount. Most pronounced at this stage is staining in the developing lungs (open arrowheads). X-gal staining cells are clearly associated with the glandular buds of the lung, but it is not possible to identify these cells in the whole mount. The only non-cardiovascular cells which exhibit X-gal staining are cells in the regions of ossification, such as in the proximal ribs shown here. Photographed at 50x. (13F) Embryo at 13.5 days, stained as whole mount, sectioned, counterstained with nuclear fast red. X-gal staining in lung tissue shown here is associated with endothelial cells, as seen in vascular channels cut in transverse (arrow) and longitudinal (arrowhead) planes. Staining is not associated with bronchial cells. Section was photographed at 400x. (13G) Cross-section through a valve forming in the outflow tract of a 13.5 day embryo. Endothelial cells in blood vessel wall are undergoing an epithelial-mesenchymal transformation, leading to formation of the valve tissue. Stained cells are seen within

the forming valve structure, indicating that these cells continue to express the *del-1* marker during this phenotypic transformation. The embryo was stained as a whole mount, sectioned, counterstained with nuclear fast red and photographed at 400x. (13H) Spiral septal formation in the outflow tract of the heart at 9.5 days pc. Endothelial cells are undergoing an epithelial-mesenchymal transformation, becoming mesenchymal in morphology and behavior. Endothelial cells continue to express the transgene marker for some time after this transformation. Section from whole mount stained embryo, 200x.

Figure 14A & 14B. Immunoblotting employing *del-1* transfected yolk sac cells. (14A) Yolk sac YS-B cells stably transfected with a eukaryotic expression vector encoding the murine major form of *del-1*(+), or an empty expression vector(-) were selected and evaluated as pools for expression of Del-1 protein. Protein was isolated from cells lysed in cell lysis buffer (Lysis) or standard Laemmli gel loading buffer (Laemmli), or from the extracellular matrix remaining after transfected cells were removed from the culture dish (ECM). The dominant band corresponds to a molecular weight of 52 kilodaltons (kDa). Lower molecular weight bands most likely represent protein degradation products, although the use of alternative translation initiation sites is also possible. (14B) YS-B cells were stably transfected with the *del-1* expression construct, or the empty expression plasmid,

and selected as individual clones. Clones expressing *del-1* were selected for varying levels of protein production, as assayed by western blot analysis of extracellular matrix protein. Clone L10 shows the highest level of *del-1* mRNA, clones L13 and L14 have an intermediate amount of message, and a negative control clone does not express *del-1*.

Figure 15A-15B. Immunostaining of yolk sac cells. (15A) *del-1* transfected yolk sac cells and the extracellular matrix are stained with anti-Del-1 antibody. The arrows indicate cell membrane staining. (15B) Mock-transfected yolk sac cells are not stained with antibody.

Figure 16. Immunostaining of Del-1 in the developing bone (vertebral column) of a 13.5 day mouse embryo. The laquanae within the bone are structures composed of extracellular matrix proteins and they are stained for Del-1.

Figure 17. Immunostaining of human glioma grown in nude mice. (17A) tumor cells are stained with anti-Del-1 antibody. Polarized staining pattern is observed (arrows). (17B) a blood vessel is stained with anti-Del-1 within the tumor.

Figure 18A-18H. (18A) The parental yolk sac cell line YS-B under routine culture conditions. Phase contrast, photo 100x. (18B) YS-B cells after 24 hrs on "MATRIGEL" show a pattern of vascular morphogenesis. Cells were stained with toluidine blue. Brightfield, photo

40x. (18C) Negative control transfectants form a vascular network on "MATRIGEL" after 24 hours. Light areas represent organized cells; photographed under dark field illumination at 50x. (18D) Yolk sac transfectant, clone L10, after 24 hrs on "MATRIGEL" shows no evidence of vascular formation, cells instead produce numerous aggregates. Darkfield illumination, photo 50x. (18E) Parental yolk sac YS-B cells grown on a matrix produced by negative control transfectants make a complex structural network. Light areas represent organized cells; photographed under dark field illumination at 30x. (18F) Parental YS-B cells grown on a matrix produced by *del-1* transfectants. Cells are forming a dense monolayer, with no evidence of organization. Photographed under darkfield illumination at 30x. (18G) Aggregates of negative control transfected yolk sac cells are placed onto polymerized "MATRIGEL". After 24 hrs, cells show sprouting angiogenesis. Photographed under phase contrast, at 100x. (18H) Aggregates of *del-1* transfected yolk sac clone L10 are placed onto polymerized "MATRIGEL" as in 18G. Photographed after 24 hrs (100x), these cells show no evidence of sprouting.

Figure 19. The binding of murine recombinant Del-1 to HUVEC is inhibited by an anti-$\alpha V\beta 3$ antibody. The relative cell number of HUVEC adhered to plates coated with recombinant Del-1 is shown in the presence of various antibodies.

Figure 20. The binding of murine recombinant Del-1 to HUVEC is inhibited by RGD peptides. The relative cell number of HUVEC adhered to plates coated with recombinant Del-1 is shown in the presence of RGD and RGE peptides at 10 μg/ml.

Figure 21A & 21B Two ideograms illustrating the chromosomal position of P1 clone 10043 at 5q14. (21A) nomenclature for human chromosomes adopted from the International System for Human Cytogenetic Nomenclature (1985). (21B) an ideogram adopted from *Cytogenet. Cell Genet.* 65:206-219 (1994) which shows the relative band positions and arm ratios derived from actual chromosome measurements.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a novel family of genes herein referred to as *del-1*. Described below are methods for cloning members of this gene family, characteristics of a murine member and its human homolog, expression of recombinant gene products, and methods of using the gene and its gene product. Structurally, members of this gene family contain three EGF-like domains and two discoidin I/factor VIII-like domains.

The overall structure of the *del-1* molecule is similar to the milk fat globule membrane protein (MFG-E8) (Stubbs et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:8417). MFG-E8 is highly expressed by a large portion of human breast tumors as well as by lactating mammary epithelial cells. It consists of two tandem EGF-like domains followed by two discoidin I/factor VIII-like domains. The function of MFG-E8 is not known but it has been shown to associate closely with cell membranes and has been investigated as a target for antibody-based tumor imaging techniques. The observed association of MFG-E8 with cell membranes indicates the potential use of

antibodies against Del-1 to identify and sort endothelial cells from mixed cell populations, and to target tumor cells that express Del-1 for diagnosis and therapy.

The second EGF-like repeat of MFG-E8 contains the amino acid sequence arg-gly-asp (RGD) in the same position as the second EGF-like repeat of Del-1. The RGD sequence has been shown to be a cell binding site for fibronectin, discoidin I, nidogen/entactin, and tenascin (Anderson, 1990, *Experientia* 46:2). The binding of fibronectin to cell surface integrin molecules through the RGD sequence has been extensively studied (Main et al., 1992, *Cell* 71:671; Hynes, 1992, *Cell* 69:11). Integrins appear to be the major receptors by which cells attach to extracellular matrices. Substrate binding to integrins has been shown to initiate signal transduction leading to events such as tyrosine phosphorylation, cytoplasmic alkalinization, activation of secretion and differentiation (Hynes, 1992, *Cell* 69:11). The presence of the RGD sequence in Del-1 indicates that this portion of the molecule may bind cell surface integrins, possibly triggering certain developmental events. In particular, Del-1 is shown to bind to integrin $\alpha V\beta 3$ on endothelial cells. In several cases, synthetic peptides containing the RGD sequence have been shown to compete with native protein for integrin binding and prevent the initiation of downstream events (Brooks et al., 1994, Cell 79:1157).

For clarity of discussion, the invention is described in the subsections below by way of example for the *del-1* genes and their products in mice and in humans. However, the findings disclosed herein may be analogously applied to other members of the *del-1* family in all species.

5.1. <u>THE *DEL-1* CODING SEQUENCE</u>

The present invention relates to nucleic acid molecules and polypeptides of the *del-1* gene family. In a specific embodiment by way of example in Section 6, <u>infra</u>, murine and human *del-1* nucleic acid molecules were cloned, and their nucleotide and deduced amino acid sequences characterized.

Both the nucleotide coding sequence and deduced amino acid sequence of *del-1* are unique. In accordance with the invention, any nucleotide sequence which encodes the amino acid sequence of the *del-1* gene product can be used to generate recombinant molecules which direct the expression of *del-1* gene.

Enhancer trapping is a strategy which has been successfully employed in genetic analysis in Drosophila but is also applicable to higher organisms. This method identifies regulatory regions in genomic loci through their influence on reporter genes (Okane et al., 1987, *Proc. Natl. Acad. Sci. U.S.A.* 84:9123-9127). The reporter gene, as a transcriptional unit under the control of a weak constitutively expressed eukaryotic promoter, is introduced into a large number of organisms. The offsprings of these organisms are then screened by analysis of the pattern of reporter gene expression. Lines which show expression in the appropriate cells at the appropriate time are maintained for further study. This strategy has successfully identified a number of loci in Drosophila involved in complex developmental processes.

Enhancer trap experiments have been employed in mice to a limited extent (Allen et al., 1988, *Nature* 333:852-855). A number of such experiments were through fortuitous integration of a reporter gene into a locus of interest (Kothary et al., 1988, *Nature* 335:435-437). Using this method coupled with genomic and cDNA cloning, the murine *del-1* locus associated with the transgene was identified. A genomic library is generated from the transgenic mouse, and a probe from the transgene used to isolate clones containing the transgene and sequences flanking the integration site. Characterization of the regulatory region is accomplished by employing flanking sequences in functional assays, via transfection experiments with an appropriate cell culture line, or via further transgenic experiments (Bhat et al., 1988, *Mol. Cell. Biol.* 8:3251-3259).

For analysis of the transcription unit, it is necessary to identify a region of flanking sequence which contains a portion of exon. This has been accomplished by blindly using flanking genomic sequences as probes in northern blots or zoo blots (Soinen et al., 1992, *Mechanisms of Development* 39:111-123). DNA fragments thus identified to contain exon sequence are employed as probes for cDNA cloning. Similar cloning experiments have been conducted to characterize loci inactivated by insertional mutagenesis associated with transgene integration. These experiments indicate that deletions of large regions of genomic DNA may accompany transgene integration, and that complexity of the transcription unit may greatly complicate this type of analysis (Karls et al., 1992, *Mol. Cell. Biol.* 12:3644-3652; Woychik et al., 1990, *Nature* 346:850-853).

Subsequent analysis of the *del-1* sequence has revealed both EGF-like and discoidin I/factor VIII-like domains. The shared homology between *del-1* and other known molecules is discussed in Section 6.2, *infra*. However, this molecule also contains regions of previously unreported unique nucleotide sequences. Northern blot hybridization analysis indicates that *del-1* mRNA is highly expressed in fetal cells. In addition, the *del-1* sequence is expressed in certain tumor cells.

In order to clone the full length cDNA sequence from any species encoding the entire *del-1* cDNA or to clone variant forms of the molecule, labeled DNA probes made from nucleic acid fragments corresponding to any murine and human of the partial cDNA disclosed herein may be used to screen a cDNA library. More specifically, oligonucleotides corresponding to either the 5′ or 3′ terminus of the cDNA sequence may be used to obtain longer nucleotide sequences. Briefly, the library may be plated out to yield a maximum of 30,000 pfu for each 150 mm plate. Approximately 40 plates may be screened. The plates are incubated at 37°C until the plaques reach a diameter of 0.25 mm or are just beginning to make contact with one another (3-8 hours). Nylon filters are

placed onto the soft top agarose and after 60 seconds, the filters are peeled off and floated on a DNA denaturing solution consisting of 0.4N sodium hydroxide. The filters are then immersed in neutralizing solution consisting of 1M Tris HCL, pH 7.5, before being allowed to air dry. The filters are prehybridized in casein hybridization buffer containing 10% dextran sulfate, 0.5M NaCl, 50mM Tris HCL, pH 7.5, 0.1% sodium pyrophosphate, 1% casein, 1% SDS, and denatured salmon sperm DNA at 0.5 mg/ml for 6 hours at 60°C. The radiolabelled probe is then denatured by heating to 95°C for 2 minutes and then added to the prehybridization solution containing the filters. The filters are hybridized at 60°C for 16 hours. The filters are then washed in 1X wash mix (10X wash mix contains 3M NaCl, 0.6M Tris base, and 0.02M EDTA) twice for 5 minutes each at room temperature, then in 1X wash mix containing 1% SDS at 60°C for 30 minutes, and finally in 0.3X wash mix containing 0.1% SDS at 60°C for 30 minutes. The filters are then air dried and exposed to x-ray film for autoradiography. After developing, the film is aligned with the filters to select a positive plaque. If a single, isolated positive plaque cannot be obtained, the agar plug containing the plaques will be removed and placed in lambda dilution buffer containing 0.1M NaCl, 0.01M magnesium sulfate, 0.035M Tris HCl, pH 7.5, 0.01% gelatin. The phage may then be replated and rescreened to obtain single, well isolated positive plaques. Positive plaques may be isolated and the cDNA clones sequenced using primers based on the known cDNA sequence. This step may be repeated until a full length cDNA is obtained.

It may be necessary to screen multiple cDNA libraries from different tissues to obtain a full length cDNA. In the event that it is difficult to identify cDNA clones encoding the complete 5′ terminal coding region, an often encountered situation in cDNA cloning, the RACE (Rapid Amplification of cDNA Ends) technique may be used. RACE is a proven PCR-based strategy for amplifying the 5′ end of incomplete cDNAs. 5′-RACE-Ready cDNA synthesized from human fetal liver containing

a unique anchor sequence is commercially available (Clontech). To obtain the 5′ end of the cDNA, PCR is carried out on 5′-RACE-Ready cDNA using the provided anchor primer and the 3′ primer. A secondary PCR reaction is then carried out using the anchored primer and a nested 3′ primer according to the manufacturer's instructions. Once obtained, the full length cDNA sequence may be translated into amino acid sequence and examined for certain landmarks such as a continuous open reading frame flanked by translation initiation and termination sites, EGF-like domain, discoidin I-like domain, a potential signal sequence and transmembrane domain, and finally overall structural similarity to the *del-1* genes disclosed herein.

5.2. EXPRESSION OF *DEL-1* SEQUENCE

In accordance with the invention, a *del-1* polynucleotide sequence which encodes the Del-1 protein, mutant polypeptides, peptide fragments of Del-1, Del-1 fusion proteins or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of Del-1 protein, Del-1 peptide fragments, fusion proteins or a functional equivalent thereof, in appropriate host cells. Such *del-1* polynucleotide sequences, as well as other polynucleotides which selectively hybridize to at least a part of such *del-1* polynucleotides or their complements, may also be used in nucleic acid hybridization assays, Southern and Northern blot analyses, etc.

Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence, may be used in the practice of the invention for the cloning and expression of the Del-1 protein. Such DNA sequences include those which are capable of hybridizing to the murine and/or human *del-1* sequences under stringent conditions. The phrase "stringent conditions" as used herein refers to those hybridizing conditions that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M

sodium citrate/0.1% SDS at 50°C.; (2) employ during hybridization a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M Sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS.

Altered DNA sequences which may be used in accordance with the invention include deletions, additions or substitutions of different nucleotide residues resulting in a sequence that encodes the same or a functionally equivalent gene product. The gene product itself may contain deletions, additions or substitutions of amino acid residues within a Del-1 sequence, which result in a silent change thus producing a functionally equivalent Del-1 protein. Such amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine, histidine and arginine; amino acids with uncharged polar head groups having similar hydrophilicity values include the following: glycine, asparagine, glutamine, serine, threonine, tyrosine; and amino acids with nonpolar head groups include alanine, valine, isoleucine, leucine, phenylalanine, proline, methionine, tryptophan.

The DNA sequences of the invention may be engineered in order to alter a *del-1* coding sequence for a variety of ends, including but not limited to, alterations which modify processing and expression of the gene product. For example, mutations may be introduced using techniques which are well known in the art, *e.g.*, site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, phosphorylation, etc.

Based on the domain organization of the Del-1 protein, a large number of Del-1 mutant polypeptides can be constructed by rearranging the nucleotide sequences that encode the Del-1 domains. Since the EGF-like domains of Del-1 are known to be involved in protein binding, Del-1 may directly bind to other cell surface receptors or extracellular matrix proteins via these domains, thereby controlling cell fate determination or differentiation in a manner similar to Notch and Notch ligands. Additionally, the RGD sequence in the second EGF-like domain is known to bind to certain integrins, thus Del-1 may regulate cell adhesiveness, migration, differentiation and viability via this sequence. The discoidin I-like domains of Del-1 are involved in a separate type of cell binding activity. In accordance with the observed properties of Factors V and VIII, Del-1 may directly bind proteoglycans in the extracellular matrix or on the cell surface via those domains. Therefore, the combination of various domains of full-length Del-1 permits the molecule to perform diverse types of binding. For example, the major form of Del-1 may be able to cluster integrin receptors by way of both EGF-like and discoidin I-like domains. In contrast, smaller fragments of Del-1 or its minor form would bind integrins without the ability to induce receptor clustering, and thus induce alternative signals to cells.

In view of the foregoing, the Del-1 mutant polypeptides can be generated and their functional activities compared. In addition to the minor form, Del-1 mutants may be constructed to contain only the EGF-like or discoidin I-like domains. Additionally, smaller polypeptides can be made from constructs that contain any one of the EGF-like and discoidin I-like domains.

In another embodiment of the invention, a *del-1* or a modified *del-1* sequence may be ligated to a heterologous sequence to encode a fusion protein. For example, for screening of peptide libraries for molecules that bind Del-1, it may be useful to encode a chimeric Del-1 protein expressing a heterologous epitope that is recognized by a

commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between a Del-1 sequence and the heterologous protein sequence, so that the Del-1 may be cleaved away from the heterologous moiety.

In an alternate embodiment of the invention, the coding sequence of Del-1 could be synthesized in whole or in part, using chemical methods well known in the art. See, for example, Caruthers *et al.*, 1980, *Nuc. Acids Res. Symp. Ser.* 7:215-233; Crea and Horn, 180, *Nuc. Acids Res. 9(10)*:2331; Matteucci and Caruthers, 1980, *Tetrahedron Letter 21*:719; and Chow and Kempe, 1981, *Nuc. Acids Res. 9(12)*:2807-2817. Alternatively, the protein itself could be produced using chemical methods to synthesize an Del-1 amino acid sequence in whole or in part. For example, peptides can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography. (*e.g.*, see Creighton, 1983, *Proteins Structures And Molecular Principles*, W.H. Freeman and Co., N.Y. pp. 50-60). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure; see Creighton, 1983, *Proteins, Structures and Molecular Principles*, W.H. Freeman and Co., N.Y., pp. 34-49).

In order to express a biologically active Del-1, the nucleotide sequence coding for Del-1, or a functional equivalent, is inserted into an appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. The *del-1* gene products as well as host cells or cell lines transfected or transformed with recombinant *del-1* expression vectors can be used for a variety of purposes. These include but are not limited to generating antibodies (*i.e.*, monoclonal or polyclonal) that competitively inhibit activity of Del-1 protein and neutralize its activity; and antibodies that mimic the activity of Del-1 binding partners such as a receptor. Anti-Del-1 antibodies may be used in detecting and quantifying expression of Del-1 levels in cells

and tissues such as endothelial cells and certain tumor cells, as well as isolating Del-1-positive cells.

5.3. EXPRESSION SYSTEMS

Methods which are well known to those skilled in the art can be used to construct expression vectors containing the *del-1* coding sequence and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Sambrook et al., 1989, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y. and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y.

A variety of host-expression vector systems may be utilized to express the *del-1* coding sequence. These include but are not limited to microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing the *del-1* coding sequence; yeast transformed with recombinant yeast expression vectors containing the *del-1* coding sequence; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the *del-1* coding sequence; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing the *del-1* coding sequence; or animal cell systems. The expression elements of these systems vary in their strength and specificities. Depending on the host/vector system utilized, any of a number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage λ, plac, ptrp, ptac (ptrp-lac hybrid promoter; cytomegalovirus promoter) and the like may be used; when cloning in insect

cell systems, promoters such as the baculovirus polyhedrin promoter may be used; when cloning in plant cell systems, promoters derived from the genome of plant cells (e.g., heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll α/β binding protein) or from plant viruses (e.g., the 35S RNA promoter of CaMV; the coat protein promoter of TMV) may be used; when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used; when generating cell lines that contain multiple copies of the *del-1* DNA, SV40-, BPV- and EBV-based vectors may be used with an appropriate selectable marker.

In bacterial systems a number of expression vectors may be advantageously selected depending upon the use intended for the *del-1* expressed. For example, when large quantities of *del-1* are to be produced for the generation of antibodies or to screen peptide libraries, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include but are not limited to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which the *del-1* coding sequence may be ligated into the vector in frame with the *lacZ* coding region so that a hybrid AS-*lacZ* protein is produced; pIN vectors (Inouye & Inouye, 1985, Nucleic acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety. In particular, murine *del-1* major and minor coding sequences have been

inserted in pET28a (Novagen Inc.) which contains a T7 promoter, and pMALC2 (New England Biolabs). These vectors encode fusion proteins which can be readily purified.

In yeast, a number of vectors containing constitutive or inducible promoters may be used. For a review see, Current Protocols in Molecular Biology, Vol. 2, 1988, Ed. Ausubel et al., Greene Publish. Assoc. & Wiley Interscience, Ch. 13; Grant et al., 1987, Expression and Secretion Vectors for Yeast, in Methods in Enzymology, Eds. Wu & Grossman, 1987, Acad. Press, N.Y., Vol. 153, pp. 516-544; Glover, 1986, DNA Cloning, Vol. II, IRL Press, Wash., D.C., Ch. 3; and Bitter, 1987, Heterologous Gene Expression in Yeast, Methods in Enzymology, Eds. Berger & Kimmel, Acad. Press, N.Y., Vol. 152, pp. 673-684; and The Molecular Biology of the Yeast Saccharomyces, 1982, Eds. Strathern et al., Cold Spring Harbor Press, Vols. I and II.

In cases where plant expression vectors are used, the expression of the *del-1* coding sequence may be driven by any of a number of promoters. For example, viral promoters such as the 35S RNA and 19S RNA promoters of CaMV (Brisson et al., 1984, Nature 310:511-514), or the coat protein promoter of TMV (Takamatsu et al., 1987, EMBO J. 6:307-311) may be used; alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi et al., 1984, EMBO J. 3:1671-1680; Broglie et al., 1984, Science 224:838-843); or heat shock promoters, e.g., soybean hsp17.5-E or hsp17.3-B (Gurley et al., 1986, Mol. Cell. Biol. 6:559-565) may be used. These constructs can be introduced into plant cells using Ti plasmids, Ri plasmids, plant virus vectors, direct DNA transformation, microinjection, electroporation, etc. For reviews of such techniques see, for example, Weissbach & Weissbach, 1988, Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey, 1988, Plant Molecular Biology, 2d Ed., Blackie, London, Ch. 7-9.

An alternative expression system which could be used to express *del-1* is an insect system. In one such system, *Autographa californica* nuclear polyhidrosis virus (AcNPV) is

used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The *del-1* coding sequence may be cloned into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of the *del-1* coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (e.g., see Smith et al., 1983, J. Viol. 46:584; Smith, U.S. Patent No. 4,215,051). A commercially available baculovirus expression vector pFastBac 1 (Gibco BRL, Inc.) has been constructed to contain the murine *del-1* coding sequence.

In mammalian host cells, a number of viral based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the *del-1* coding sequence may be ligated to an adenovirus transcription/translation control complex, *e.g.*, the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (*e.g.*, region E1 or E3) will result in a recombinant virus that is viable and capable of expressing *del-1* in infected hosts. (*e.g.*, See Logan & Shenk, 1984, Proc. Natl. Acad. Sci. USA 81:3655-3659). Alternatively, the vaccinia 7.5K promoter may be used. (See, e.g., Mackett et al., 1982, Proc. Natl. Acad. Sci. USA 79:7415-7419; Mackett et al., 1984, J. Virol. 49:857-864; Panicali et al., 1982, Proc. Natl. Acad. Sci. USA 79:4927-4931).

Additionally, both the murine *del-1* and human coding sequences have been inserted in a mammalian expression vector, pcDNA3 (Invitrogen, Inc.), which is under the control of the cytomegalovirus promoter. Regulatable expression vectors such as the tetracycline inducible vectors may also

be used to express the coding sequences in a controlled fashion.

Specific initiation signals may also be required for efficient translation of inserted *del-1* coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where the entire *del-1* gene, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of the *del-1* coding sequence is inserted, exogenous translational control signals, including the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the *del-1* coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., 1987, Methods in Enzymol. 153:516-544).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. The presence of several consensus N-glycosylation sites in the *del-1* extracellular domain support the possibility that proper modification may be important for Del-1 function. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such

mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, WI38, yolk sac cells, etc.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the *del-1* may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with the *del-1* DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the Del-1 protein on the cell surface. Such engineered cell lines are particularly useful in screening for molecules or drugs that affect *del-1* function.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell 22:817) genes can be employed in tk^-, $hgprt^-$ or $aprt^-$ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for *dhfr*, which confers resistance to methotrexate (Wigler, et al., 1980, Natl. Acad. Sci. USA 77:3567; O'Hare, et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); *gpt*, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981), Proc. Natl. Acad. Sci. USA 78:2072); *neo*, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, J. Mol. Biol. 150:1); and

hygro, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30:147) genes. Recently, additional selectable genes have been described, namely *trpB*, which allows cells to utilize indole in place of tryptophan; *hisD*, which allows cells to utilize histinol in place of histidine (Hartman & Mulligan, 1988, Proc. Natl. Acad. Sci. USA 85:8047); and *ODC* (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue L., 1987, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.).

5.4. IDENTIFICATION OF CELLS THAT EXPRESS *DEL-1*

The host cells which contain the coding sequence and which express a biologically active *del-1* gene product or fragments thereof may be identified by at least four general approaches; (a) DNA-DNA or DNA-RNA hybridization; (b) the presence or absence of "marker" gene functions; (c) assessing the level of transcription as measured by the expression of *del-1* mRNA transcripts in the host cell; and (d) detection of the gene product as measured by immunoassay or by its biological activity. Prior to the identification of gene expression, the host cells may be first mutagenized in an effort to increase the level of expression of *del-1*, especially in cell lines that produce low amounts of *del-1*.

In the first approach, the presence of the *del-1* coding sequence inserted in the expression vector can be detected by DNA-DNA or DNA-RNA hybridization using probes comprising nucleotide sequences that are homologous to the *del-1* coding sequence, respectively, or portions or derivatives thereof.

In the second approach, the recombinant expression vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, resistance to methotrexate, transformation phenotype, occlusion body formation in baculovirus, etc.). For example, if the *del-1* coding sequence is inserted within a marker gene

sequence of the vector, recombinants containing the *del-1* coding sequence can be identified by the absence of the marker gene function. Alternatively, a marker gene can be placed in tandem with the *del-1* sequence under the control of the same or different promoter used to control the expression of the *del-1* coding sequence. Expression of the marker in response to induction or selection indicates expression of the *del-1* coding sequence.

In the third approach, transcriptional activity for the *del-1* coding region can be assessed by hybridization assays. For example, RNA can be isolated and analyzed by Northern blot using a probe homologous to the *del-1* coding sequence or particular portions thereof. Alternatively, total nucleic acids of the host cell may be extracted and assayed for hybridization to such probes. Additionally, RT-PCR may be used to detect low levels of gene expression.

In the fourth approach, the expression of the Del-1 protein product can be assessed immunologically, for example by Western blots, immunoassays such as radioimmuno-precipitation, enzyme-linked immunoassays and the like. This can be achieved by using an anti-Del-1 antibody and a Del-1 binding partner such as $\alpha V\beta 3$. Alternatively, the biologic activities of Del-1 can be determmined by assaying its ability to inhibit vascular morphogenesis of endothelial cells.

5.5. <u>USES OF *DEL-1* ENGINEERED CELL LINES</u>

In an embodiment of the invention, the Del-1 protein and/or cell lines that express Del-1 may be used to screen for antibodies, peptides, small molecules natural and synthetic compounds or other cell bound or soluble molecules that bind to the Del-1 protein. For example, anti-Del-1 antibodies may be used to inhibit or stimulate Del-1 function. Alternatively, screening of peptide libraries with recombinantly expressed soluble Del-1 protein or cell lines expressing Del-1 protein may be useful for identification of therapeutic molecules that function by inhibiting or

stimulating the biological activity of Del-1. The uses of the Del-1 protein and engineered cell lines, described in the subsections below, may be employed equally well for other members of the *del-1* gene family in various species.

In an embodiment of the invention, engineered cell lines which express most of the *del-1* coding region or a portion of it fused to another molecule such as the immunoglobulin constant region (Hollenbaugh and Aruffo, 1992, Current Protocols in Immunology, Unit 10.19; Aruffo et al., 1990, Cell 61:1303) may be utilized to produce a soluble molecule to screen and identify its binding partners. The soluble protein or fusion protein may be used to identify such a molecule in binding assays, affinity chromatography, immunoprecipitation, Western blot, and the like. Alternatively, portions of *del-1* may be fused to the coding sequence of the EGF receptor transmembrane and cytoplasmic regions. Assuming that Del-1 can function as a cell-bound receptor, this approach provides for the use of the EGF receptor signal transduction pathway as a means for detecting molecules that bind to Del-1 in a manner capable of triggering an intracellular signal. On the other hand, Del-1 may be used as a soluble factor in binding to cell lines that express specific known receptors such as integrins. Synthetic compounds, natural products, and other sources of potentially biologically active materials can be screened in assays that are well known in the art.

Random peptide libraries consisting of all possible combinations of amino acids attached to a solid phase support may be used to identify peptides that are able to bind to the ligand binding site of a given receptor or other functional domains of a receptor such as kinase domains (Lam, K.S. et al., 1991, Nature 354: 82-84). The screening of peptide libraries may have therapeutic value in the discovery of pharmaceutical agents that stimulate or inhibit the biological activity of receptors through their interactions with the given receptor.

Identification of molecules that are able to bind to the Del-1 protein may be accomplished by screening a peptide library with recombinant soluble Del-1 protein. Methods for expression and purification of Del-1 are described in Section 5.2, *supra*, and may be used to express recombinant full length *del-1* or fragments of *del-1* depending on the functional domains of interest. For example, the EGF-like and discoidin I/factor VIII domains of *del-1* may be separately expressed and used to screen peptide libraries.

To identify and isolate the peptide/solid phase support that interacts and forms a complex with Del-1, it is necessary to label or "tag" the Del-1 molecule. The Del-1 protein may be conjugated to enzymes such as alkaline phosphatase or horseradish peroxidase or to other reagents such as fluorescent labels which may include fluorescein isothiocyanate (FITC), phycoerythrin (PE) or rhodamine. Conjugation of any given label to Del-1 may be performed using techniques that are well known in the art. Alternatively, *del-1* expression vectors may be engineered to express a chimeric Del-1 protein containing an epitope for which a commercially available antibody exist. The epitope specific antibody may be tagged using methods well known in the art including labeling with enzymes, fluorescent dyes or colored or magnetic beads.

The "tagged" Del-1 conjugate is incubated with the random peptide library for 30 minutes to one hour at 22°C to allow complex formation between Del-1 and peptide species within the library. The library is then washed to remove any unbound protein. If Del-1 has been conjugated to alkaline phosphatase or horseradish peroxidase the whole library is poured into a petri dish containing substrates for either alkaline phosphatase or peroxidase, for example, 5-bromo-4-chloro-3-indoyl phosphate (BCIP) or 3,3',4,4"-diaminobenzidine (DAB), respectively. After incubating for several minutes, the peptide/solid phase-Del-1 complex changes color, and can be easily identified and isolated physically under a dissecting microscope with a

micromanipulator. If a fluorescent tagged Del-1 molecule has been used, complexes may be isolated by fluorescence activated sorting. If a chimeric Del-1 protein expressing a heterologous epitope has been used, detection of the peptide/Del-1 complex may be accomplished by using a labeled epitope specific antibody. Once isolated, the identity of the peptide attached to the solid phase support may be determined by peptide sequencing.

In addition to using soluble Del-1 molecules, in another embodiment, it is possible to detect peptides that bind to cell surface receptors using intact cells. The use of intact cells is preferred for use with receptors that are multi-subunits or labile or with receptors that require the lipid domain of the cell membrane to be functional. Methods for generating cell lines expressing *del-1* are described in Section 5.3. The cells used in this technique may be either live or fixed cells. The cells may be incubated with the random peptide library and bind to certain peptides in the library to form a "rosette" between the target cells and the relevant solid phase support/peptide. The rosette can thereafter be isolated by differential centrifugation or removed physically under a dissecting microscope.

As an alternative to whole cell assays for membrane bound receptors or receptors that require the lipid domain of the cell membrane to be functional, the receptor molecules can be reconstituted into liposomes where label or "tag" can be attached.

Various procedures known in the art may be used for the production of antibodies to epitopes of the natural and recombinantly produced Del-1 protein. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments and fragments produced by an Fab expression library. Neutralizing antibodies i.e., those which compete for the ligand binding site of the Del-1 protein are especially preferred for diagnostics and therapeutics.

Monoclonal antibodies that bind Del-1 may be radioactively labeled allowing one to follow their location and distribution in the body after injection. Radioisotope tagged antibodies may be used as a non-invasive diagnostic tool for imaging *de novo* cells of tumors and metastases.

Immunotoxins may also be designed which target cytotoxic agents to specific sites in the body. For example, high affinity Del-1 specific monoclonal antibodies may be covalently complexed to bacterial or plant toxins, such as diphtheria toxin, ricin. A general method of preparation of antibody/hybrid molecules may involve use of thiol-crosslinking reagents such as SPDP, which attack the primary amino groups on the antibody and by disulfide exchange, attach the toxin to the antibody. The hybrid antibodies may be used to specifically eliminate Del-1 expressing tumor cells.

For the production of antibodies, various host animals may be immunized by injection with the recombinant or naturally purified Del-1 protein, fusion protein or peptides, including but not limited to rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum*.

Monoclonal antibodies to Del-1 may be prepared by using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Kohler and Milstein, (Nature, 1975, 256:495-497), the human B-cell hybridoma technique (Kosbor et al., 1983, Immunology Today, 4:72; Cote et al., 1983, Proc. Natl. Acad. Sci., 80:2026-2030) and the EBV-hybridoma technique (Cole et al., 1985, Monoclonal Antibodies and Cancer Therapy,

Alan R. Liss, Inc., pp. 77-96). In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci., 81:6851-6855; Neuberger et al., 1984, Nature, 312:604-608; Takeda et al., 1985, Nature, 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce Del-1-specific single chain antibodies.

Hybridomas may be screened using enzyme-linked immunosorbent assays (ELISA) in order to detect cultures secreting antibodies specific for refolded recombinant Del-1. Cultures may also be screened by ELISA to identify those cultures secreting antibodies specific for mammalian-produced Del-1. Confirmation of antibody specificity may be obtained by western blot using the same antigens. Subsequent ELISA testing may use recombinant Del-1 fragments to identify the specific portion of the Del-1 molecule with which a monoclonal antibody binds. Additional testing may be used to identify monoclonal antibodies with desired functional characteristics such as staining of histological sections, immunoprecipitation of Del-1, or neutralization of Del-1 activity. Determination of the monoclonal antibody isotype may be accomplished by ELISA, thus providing additional information concerning purification or function.

Antibody fragments which contain specific binding sites of Del-1 may be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed (Huse et al., 1989, Science, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity to Del-1. Anti-Del-1

antibodies may be used to isolate Del-1-expressing cells or eliminate such cells from a cell mixture.

5.6. USES OF *DEL-1* POLYNUCLEOTIDE

A *del-1* polynucleotide may be used for diagnostic and/or therapeutic purposes. For diagnostic purposes, a *del-1* polynucleotide may be used to detect *del-1* gene expression or aberrant *del-1* gene expression in disease states. Included in the scope of the invention are oligonucleotide sequences, that include antisense RNA and DNA molecules and ribozymes, that function to inhibit translation of *del-1*.

5.6.1. DIAGNOSTIC USES OF A *DEL-1* POLYNUCLEOTIDE

A *del-1* polynucleotide may have a number of uses for the diagnosis of diseases resulting from aberrant expression of *del-1*. For example, the *del-1* DNA sequence may be used in hybridization assays of biopsies or autopsies to diagnose abnormalities of *del-1* expression; *e.g.*, Southern or Northern analysis, including *in situ* hybridization assays. Such techniques are well known in the art, and are in fact the basis of many commercially available diagnostic kits.

5.6.2. THERAPEUTIC USES OF A *DEL-1* POLYNUCLEOTIDE

A *del-1* polynucleotide may be useful in the treatment of various abnormal conditions. By introducing gene sequences into cells, gene therapy can be used to treat conditions in which the cells do not proliferate or differentiate normally due to underexpression of normal *del-1* or expression of abnormal/inactive *del-1*. In some instances, the polynucleotide encoding a *del-1* is intended to replace or act in the place of a functionally deficient endogenous gene. Alternatively, abnormal conditions characterized by overproliferation can be treated using the gene therapy techniques described below.

Abnormal cellular proliferation is an important component of a variety of disease states. Recombinant gene therapy vectors, such as viral vectors, may be engineered to

express variant, signalling incompetent forms of Del-1 which may be used to inhibit the activity of the naturally occurring endogenous Del-1. A signalling incompetent form may be, for example, a truncated form of the protein that is lacking all or part of its signal transduction domain. Such a truncated form may participate in normal binding to a substrate but lack signal transduction activity. Thus recombinant gene therapy vectors may be used therapeutically for treatment of diseases resulting from aberrant expression or activity of an Del-1. Accordingly, the invention provides a method of inhibiting the effects of signal transduction by an endogenous Del-1 protein in a cell comprising delivering a DNA molecule encoding a signalling incompetent form of the Del-1 protein to the cell so that the signalling incompetent Del-1 protein is produced in the cell and competes with the endogenous Del-1 protein for access to molecules in the Del-1 protein signalling pathway which activate or are activated by the endogenous Del-1 protein.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adeno-associated virus, herpes viruses, or bovine papilloma virus, may be used for delivery of recombinant Del-1 into the targeted cell population. Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing an *del-1* polynucleotide sequence. See, for example, the techniques described in Maniatis *et al.*, 1989, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y. and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y. Alternatively, recombinant Del-1 molecules can be reconstituted into liposomes for delivery to target cells.

Oligonucleotide sequences, that include anti-sense RNA and DNA molecules and ribozymes that function to inhibit the translation of a *del-1* mRNA are within the scope of the invention. Anti-sense RNA and DNA molecules act to directly block the translation of mRNA by binding to targeted mRNA and preventing protein translation. In regard to antisense DNA,

oligodeoxyribonucleotides derived from the translation initiation site, *e.g.*, between -10 and +10 regions of a *del-1* nucleotide sequence, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Within the scope of the invention are engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of *del-1* RNA sequences.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features such as secondary structure that may render the oligonucleotide sequence unsuitable. The suitability of candidate targets may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

Both anti-sense RNA and DNA molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Various modifications to the DNA molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribo- or deoxy- nucleotides to the 5′ and/or 3′ ends of the molecule or the use of phosphorothioate or 2′ O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

Methods for introducing polynucleotides into such cells or tissue include methods for *in vitro* introduction of polynucleotides such as the insertion of naked polynucleotide, *i.e.*, by injection into tissue, the introduction of a *del-1* polynucleotide in a cell *ex vivo*, *i.e.*, for use in autologous cell therapy, the use of a vector such as a virus, retrovirus, phage or plasmid, etc. or techniques such as electroporation which may be used *in vivo* or *ex vivo*.

5.7. USES OF *DEL-1* PROTEIN

Analysis of β-gal expression in transgenic mice in which β-gal gene expression is controlled by the *del-1* enhancer indicates that the *del-1* gene is activated in endothelial cells undergoing vasculogenesis. Vasculogenesis refers to the development of blood vessels *de novo* from embryonic precursor cells. The related process of angiogenesis is the process through which existing blood vessels arise by outgrowth from preexisting ones. Vasculogenesis is limited to the embryo while angiogenesis continues throughout life as a wound healing response or to increase oxygenation of chronically stressed tissues (Pardanaud et al., 1989 *Development* 105:473; Granger 1994, *Cell and Mol. Biol. Res.* 40:81).

It is likely that Del-1 functions during embryonic vasculogenesis and in angiogenesis. For therapeutic use, it is essential that Del-1, portions of Del-1 or antibodies that block Del-1, may interact with angiogenic cells since it is stimulation or inhibition of these cells that is clinically

relevant. Manipulation of Del-1 function may have significant effects on angiogenesis if Del-1 normally participates in this process.

The working examples in Sections 9 and 10 demonstrate that Del-1 exhibits an inhibitory effect on angiogenesis, which may be mediated by its interaction with $\alpha V\beta 3$-expressing endothelial cells. Del-1 protein or recombinant proteins consisting of portions of Del-1 may function to suppress angiogenesis or induce endothelial cell apoptosis. This function could be clinically useful to prevent neovascularization of tissues such as tumor nodules. It has been demonstrated that inhibition of angiogenesis is useful in preventing tumor metastases (Fidler and Ellis, 1994, *Cell* 79:185). Recently, O'Reilly et al (1994, *Cell* 79:315) reported that a novel angiogenesis inhibitor isolated from tumor-bearing mice, angiostatin, specifically inhibited endothelial cell proliferation. *In vivo*, angiostatin was a potent inhibitor of neovascularization and growth of tumor metastases. In a related report, Brooks et al (1994, *Cell* 79:115) showed that integrin antagonists promoted tumor regression by inducing apoptosis of angiogenic blood vessels. These integrin antagonists included cyclic peptides containing an RGD amino acid sequence. Since Del-1 contains an RGD sequence, the use of this portion of the Del-1 molecule may have similar effects.

Manipulation of the discoidin I/factor VIII-like domains of Del-1 may also be used to inhibit angiogenesis. Apolipoprotein E (ApoE) has been shown to inhibit basic fibroblast growth factor (bFGF)-stimulated proliferation of endothelial cells *in vitro* (Vogel et al., 1994, *J. Cell. Biochem.* 54:299). This effect could also be produced with synthetic peptides based on a portion of the ApoE sequence. These results could be due to direct competition of ApoE with growth factors for binding to heparin sulfate proteoglycans, or through disruption by ApoE of cell-matrix interactions. It has been proposed that discoidin I/factor VIII-like domains such as those in Del-1 bind to proteoglycans. In

addition, Del-1 is similar in structure to a number of extracellular matrix proteins. Thus, Del-1 may be manipulated to effect the activity of growth factors such as bFGF or to alter interactions between endothelial cells and the extracellular matrix.

The anti-angiogenic activity of Del-1 may be used to treat abnormal conditions that result from angiogenesis. These conditions include, but are not limited to, cancer, diabetic retinopathy, rheumatoid arthritis and endometriosis. Additionally, the removal or inhibition of Del-1 in situations where it naturally inhibits blood vessel formation may be used to promote angiogenesis. These conditions inlcude, but are not limited to, cardiac ischemia, thrombotic stroke, would healing and peripheral vascular disease. Furthermore, Del-1 may be used to stimulate bone formation.

6. EXAMPLE: MOLECULAR CLONING OF HUMAN AND MURINE *DEL-1* NUCLEOTIDE SEQUENCES

6.1. MATERIALS AND METHODS

6.1.1. GENERATION OF TRANSGENIC MICE

The SLM275 transgenic mouse line was generated in a C57BL6xDBA/F1 background, and the transgenic animals had been crossed back against similar B6D2F1 animals for maintenance of the line and the generation of embryos. This transgene had been maintained in the heterozygous state, and these heterozygous mice had normal breeding capacity. However, preliminary experiments indicated that these animals were not viable in the homozygous state.

6.1.2. MOLECULAR CLONING OF *DEL-1*

A genomic library was constructed from high molecular weight DNA isolated from the kidney of a SLM275 transgenic animal. This DNA was subjected to partial digestion with Sau3A to obtain an average size of 20 kb, subjected to a partial fill-in reaction, and then cloned into a similarly treated lambdaphage vector (lambdaFix,

Stratagene). The library constructed in this fashion had a base of approximately 2 million clones. These clones were amplified and the library stored at -70°C. A 200 basepair (bp) probe derived from the SV40 polyadenylation signal of the transgene was used as a probe and allowed the isolation of 12 lambdaphage clones. Six of these clones were randomly chosen for further investigation. These clones were mapped, and restriction fragments which did not contain transgene sequence identified. The clones were divided into two groups on the basis of common non-transgenic fragments. One such fragment from the first group of phage allowed specific hybridization to genomic blots and provided evidence that it was derived from a region adjacent to the integration site. Genomic DNA from a non-transgenic mouse of the same genetic background (B6D2F1) was compared to that of a SLM275 transgene animal by hybridization to this probe. Rearranged bands representing fragments disrupted by transgene integration were seen in the SLM275 lanes with both EcoR1 and BamH1 digests. The flanking sequence probe was employed to screen a commercially available lambdaFixII genomic library constructed from the 129SV mouse strain (Stratagene).

A murine cDNA fragment was used as a probe to identify cDNA clones of its human homolog. The probe corresponded to nucleotides 1249 through 1566 in the murine *del-1* major sequence. Human cDNA clones were isolated from a human fetal lung cDNA library (Clonetech, Inc.) following standard procedures.

6.2. <u>RESULTS</u>

A transgenic mouse line was created through a fortuitous enhancer trap event. The original studies were designed to map the cell-specific and developmental-specific regulatory regions of the mouse SPARC promoter, 2.2 kilobases (kb) of the SPARC 5′ flanking sequence were placed upstream of the *E. coli lacZ* (beta-galactosidase or β-gal) reporter gene. The mouse SPARC gene is normally expressed in a wide variety of adult and embryonic cells which synthesize a specific

extracellular matrix (Nomura et al., 1989, *J. Biol. Chem.* 264:12201-12207). However, one of the founder mouse lines showed a highly restricted pattern of expression quite distinct from the native SPARC gene. Expression of the *lacZ* reporter in this particular line of mice referred to as SLM275 was seen very early in cells of the endothelial lineage. Whole mount *lacZ* staining was employed for initial studies, and these embryos were subsequently sectioned and examined by light microscopy. The first cells to stain were endothelial cells forming the endocardium, the outflow tract, and the developing intervertebral vessels. Staining appeared to be predominantly restricted to endothelial cells associated with forming major blood vessels. Expression began to decline after 11.5 days pc.

The genomic region targeted by this transgene is herein referred to as *del-1*. Initial cloning experiments were aimed at isolating genomic sequences flanking the transgene integration site. A number of lambdaphage clones were isolated and mapped (Figure 1). Approximately 40 kb of the wild-type *del-1* sequence was contained in these clones. By probing Southern blots containing restriction digests of these lambdaphages with non-transgenic fragments from the SLM275 lambdaphage clones, the site of transgene integration was mapped. Insertion of the transgene complex was associated with the deletion of approximately 8 kb of DNA. There were approximately 25 kb of flanking sequence on one side of the integration, and approximately 5 kb of the other flanking sequence contained on these clones.

Exon trapping was used to evaluate genomic fragments for the presence of exons. This approach utilized a vector with a constitutive promoter driving transcription through a DNA fragment containing a splice donor site and a splice acceptor site. Between these splicing signals was a common cloning site where the genomic DNA fragment to be evaluated was cloned. Exons within this fragment would be spliced into the transcript when the construct was transfected into eukaryotic cells, such as COS cells. The transcript containing the

trapped exon sequence was rescued from the COS cells by reverse transcriptase polymerase chain reaction (RT-PCR). PCR amplified DNA was cloned and evaluated.

A 160 bp exon was trapped from a fragment of genomic DNA located approximately 10 kb from the "left" integration site. Nucleotide sequence of the trapped exon was employed to screen various nucleic acid databanks through the BLAST routine at the NCBI, revealing no other gene with significant nucleic acid homology. The deduced amino acid sequence of the single open reading frame was subsequently employed in databank searches. These revealed that the protein domain encoded in the trapped exon was similar in part to domains in a number of proteins, including Factor V, Factor VIII and discoidin I (Figure 2) (Jenny et al., 1987, *Proc. Natl. Acad. Sci. U.S.A.* 84:4846-4850; Poole et al., 1981, *J. Mol. Biol.* 153:273-289; Toole et al., 1984, *Nature* 312:342-347). The protein which was most similar was milkfat globule protein, which had been found on the surface of mammary epithelial cells (1994, WO 94/11508). It has been hypothesized that the discoidin I-like domain in this protein allows it to localize to the surface of the epithelial cell (Larocca et al., 1991, *Cancer Res.* 51:4994-4998; Stubbs et al., 1990, *Proc. Natl. Acad. Sci. U.S.A.* 87:8417-8421). The homologous regions of Factor V and Factor VIII have been implicated in their interaction with phospholipids on the surface of endothelial cells and platelets (Jenny et al., 1987, *Proc. Natl. Acad. Sci. U.S.A.* 84:4846-4850; Toole et al., 1984, *Nature* 312:342-347). Homology to the Xenopus protein A5 was also observed. A5 is a neuronal cell surface molecule which is expressed in retinal neurons and the neurons in the visual center with which the retinal neurons contact (Takagi et al., 1991, *Neuron* 7:295-307). A5 has been proposed to play a role as a neuronal recognition molecule in the development of this neural circuit, perhaps through mediating intercellular signaling. The protein for which this discoidin I-like domain was named is a protein expressed in *Dictyostelium*

discoideum, which serves an essential role in the aggregation of individual cells.

The DNA fragment encoding the trapped exon was employed as a probe in a Southern blot experiment and shown to hybridize with regions of the *del-1* locus outside of the region that was employed in the exon trap construct. Given this finding, cDNA cloning was pursued by using the exon trap probe to screen an 11.5 day embryonic mouse cDNA library. Clones were plaque purified, and inserts subcloned into plasmid for further analysis. Nucleotide sequence analysis showed that two of the embryonic cDNA clones contained the sequence of the trapped exon. Sequence from the clones was used to expand the deduced amino acid sequence of the discoidin I-like domain (Figure 2). The full nucleotide sequence of these cDNAs was analyzed and cloned into plasmid vectors which allowed the generation of cRNA transcripts for RNAse protection and in situ hybridization (Figure 3A-3E).

A human cDNA was isolated from a human fetal lung cDNA lambdaphage library purchased from Clontech Inc. (Figure 4A-4C). A portion of the mouse *del-1* cDNA was used as a probe (Figure 5). The identity of the human cDNA clone was confirmed by comparing the human and mouse DNA sequences. These clones show approximately 80% DNA sequence homology and approximately 94% amino acid sequence homology (Figure 6). These sequences are referred to as the "major" form of *del-1*. Upon initial isolation of *del-1*, standard molecular biology methods were used for isolating additional clones.

DNA sequence analysis of the human *del-1* revealed an open reading frame of 1,446 base pairs predicted to encode a 481 amino acid protein with a molecular weight of 53,797. The mouse cDNA encodes a 480 amino acid protein. Homology comparisons with DNA and protein databases indicated that the Del-1 protein was composed of three EGF-like protein domains, followed by two discoidin I/factor VIII-like domains (Figure 7). Genes similar to *del-1* included some key regulators of cell determination and differentiation such as Notch. Overall, the Del-1 protein has a structure similar to the

membrane-associated milk fat globule membrane protein, MGF-E8, which has been used to develop antibodies for imaging breast cancer (Figure 8).

A physiologic function for the Del-1 protein is implicated by the activities which have been demonstrated for EGF-like and discoidin I/factor VIII-like domains in other proteins. EGF-like domains have been shown to participate in protein-protein binding interactions, while the discoidin I-like domains of factor VIII are believed to mediate binding to cell membranes through association with negatively charged phospholipids. Thus, the Del-1 protein may generate a signal for endothelial cell determination or differentiation by binding to the membranes of precursor cells and interacting with an EGF-like domain receptor protein.

Key structural features of the open reading frame of human Del-1 include:

1) the presumed initiator methionine and putative secretion signal sequence (Figure 9)
2) the three EGF-like domains (Figure 10)
3) the two discoidin I-like domains.

Further cloning and analysis of both the human and murine *del-1* genes revealed additional variant forms. For example, a human splicing variant (Z20 clone) was obtained in which 30 bp (i.e. 10 amino acids) between the first and second EGF-like domains of the major form of *del-1* had been removed (Figure 11). In addition, a truncated version of murine *del-1* was isolated, which contained a signal peptide sequence, all three EGF-like domains and only a partial amino-terminal discoidin I/factor VIII-like domain (about 40%). This variant is referred to as murine *del-1* minor sequence, which is disclosed in Figure 12A-12E. This transcript was cloned only from mouse embryonic libraries, but was verified through cloning of several independent cDNAs.

7. EXAMPLE: TISSUE DISTRIBUTION OF *DEL-1* GENE EXPRESSION

7.1. MATERIALS AND METHODS

7.1.1. WHOLE MOUNT STAINING OF TRANSGENIC MOUSE EMBRYOS

Male transgenic animals of second or third generation had been crossed with 8-10 week B6D2F1 females, and embryos harvested at 7.5, 8.5, 9.5, 10.5, and 13.5 days. Timing was based on the convention that noon of the day of plugging was 0.5 day post-coitum (pc). Embryos were harvested, dissected free of decidua and membranes, fixed in 2% glutaraldehyde, and stained as a whole mount in a standard X-gal indicator solution according to standard protocols. An exception was that embryos older than 11.5 days were bisected which allowed better penetration of the fixative and staining solution. Stained tissues were identified in whole mount embryos by examination at 7-70x with an Olympus SZH10 stereomicroscope, and photographed under darkfield illumination. Embryos 7.5, 8.5, 9.5, and 13.5 days pc were embedded in paraffin, sectioned, counterstained with nuclear fast red and examined under brightfield with a Zeiss Axioplan microscope.

7.1.2. NORTHERN BLOT ANALYSIS

In order to study the expression of the *del-1* gene, Northern blots containing RNA obtained from a variety of human and mouse tissues (Clontech, Palo Alto, CA) were hybridized with a radiolabeled DNA probe as shown in Figure 5. In addition, adult organs, 15.5 dpc whole embryos and organs dissected from embryos were disrupted with a polytron, and RNA isolated over C_sCl gradient (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Briefly, the blots were prehybridized at 42°C for 3-6 hours in a solution containing 5X SSPE, 10X Denhardt's solution, 100 μg/ml freshly denatured, sheared salmon sperm DNA, 50% formamide (freshly deionized), and 2% SDS. The radiolabeled probe was heat denatured and added to the prehybridization mix and allowed to hybridize at 42°C for 18-24 hours with constant shaking.

The blots were rinsed in 2X SSC, 0.05% SDS several times at room temperature before being transferred to a wash solution containing 0.1X SSC, 0.1% SDS and agitated at 50°C for 40 minutes. The blots were then covered with plastic wrap, mounted on Whatman paper and exposed to x-ray film at -70°C using an intensifying screen.

7.1.3 REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION (RT-PCR)

Total RNA was isolated using standard laboratory procedures (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Approximately 1 μg of total RNA was reverse transcribed and the cDNA was amplified by PCR (Perkin Elmer, Norwalk, CT). The PCR amplification conditions were: 94°C for 30 sec, 60°C for 30 sec, 72°C for 30 sec for a total of 40 cycles. The amplified products were resolved by agarose gel electrophoresis and visualized by ethidium bromide staining. The amplimers were:

+ strand primer: ACC CAA GGG GCA AAA AGG A
- strand primer: CCT GTA ACC ATT GTG ACT G

7.2. RESULTS

Expression of *del-1* in various human and mouse tissues and cell lines was investigated by whole mount staining, Northern blot analysis and RT-PCR. Results of experiments are summarized in the subsections below.

7.2.1 EXPRESSION ANALYSIS BY HISTOCHEMISTRY

When the earliest time point was investigated by whole mount and histochemical staining in transgenic mice at day 7.5 pc, expression of the *lacZ* reporter gene was shown in cells forming the extra embryonic mesoderm (Figure 13A). These cells would form the yolk sac and give rise to cells of the blood island. Expression of the *lacZ* reporter gene in this locus is thus one of the earliest known markers of the endothelial cell lineage. The only other marker which has

been shown to be expressed in precursors of endothelial cells at this early stage of development is the receptor tyrosine kinase *flk-1* (Millauer et al., 1993, *Cell* 72:835-846). However, *del-1* expression was not found in the allantois, as with other early markers of the endothelium such as *flk-1* (Yamaguchi et al., 1993, *Development* 118:489-498).

At day 8.5, *lacZ* staining was seen in cells in the blood islands of the yolk sac. Interestingly, staining was not detected in mature endothelial cells lining the blood island, but rather in round cells found in clumps within the blood island (Figure 13B). These round cells had large nuclei and were closer in appearance to hematopoietic precursors rather than endothelial cells. This expression pattern was distinct from all other early endothelial markers. Thus, the *del-1* locus might be expressed in early embryonic cells which were precursors to both endothelial and hematopoietic lineages. In the late primitive streak stage embryo at 8.5 days pc, there was also staining of endothelial cells associated with the developing paired dorsal aortae. *LacZ* staining was seen in cells in the region of the forming heart at this stage, and these were presumably endothelial cells that would form the endocardium. By day 9.5 (10-14 somites), the endocardium and endothelial cells forming the outflow tract and aorta showed *lacZ* staining (Figure 13C, 13D). This staining persisted until day 10.5 and 11.5, and by whole mount analysis endothelial cells associated with all large vascular structures were expressing the reporter gene.

LacZ staining of embryos at day 13.5 of development was evaluated in the whole mount, and in sections made from paraffin embedded embryos. By this time, there was only patchy staining of endothelial cells in large vessels such as the aorta, whereas smaller vessels had virtually no staining (Figure 13E). The only blood vessels which showed prominent *lacZ* staining at this stage were the pulmonary capillaries. The developing pulmonary vascular network stained intensely, making the entire lung appear grossly blue-green (Figure 13E). Identification of the stained cells was made by

microscopy of stained sections (Figure 13F). Also, visualization of X-gal stained cells forming vascular channels was possible by viewing thick sections with Nomarski differential interference contrast optics. Organ vasculature associated the liver, brain and kidney showed no staining. In the heart, there was some residual staining of endothelial cells of the atrium. The majority of endothelial cells lining the ventricle no longer stained. The striking finding in the ventricle was that the cells forming the papillary muscle and the mitral valve showed marked staining. This labeling was seen not only in the endothelial cells on the surface, but in cells forming these structures. In a similar fashion, cells in the area of the forming valves of the aorta and pulmonary showed *lacZ* activity. Again, cells in the forming valve and in the wall of the vessel were stained (Figure 13G and 13H). The only non-cardiovascular staining was observed in cells in the areas of active bone formation. In particular, staining was most prominent in the proximal portions of the ribs, vertebrae, and the limb girdles (Figure 13E). After 13.5 days, the only cells expressing the *lacZ* gene were pulmonary endothelial cells. After approximately 15.5 days of development, expression of the reporter transgene diminished and was completely negative by the time of birth.

The aforementioned observations indicate that the protein encoded by the transcription unit in the *del-1* locus is involved in early developmental processes in the cardiovascular system. This gene is not only a lineage marker, since it is expressed in restricted groups of endothelial cells in a temporally regulated fashion. The restricted expression seen at later stages indicates a connection with the origin of these endothelial cells, the mechanism of blood vessel formation, or the context-derived phenotype of these cells. Cells of the primordial endocardium express this marker, indicating a role in cardiogenesis. Most striking is the pattern of expression in the developing valvular apparatus of the heart. Competent

endothelial cells in the forming septum and valves have been shown to undergo an epithelial-mesenchymal transformation. This transformation appears to be due, at least in part, to an inductive signal, such as transforming growth factor beta 3, which is released by the myocardium (Potts et al., 1991, *Proc. Natl. Acad. Sci. U.S.A.* 88:1516-1520; Sinning et al., 1992, *Anat. Rec.* 232:285-292). Reporter gene expression in the SLM275 mouse marked the competent cells of the endocardium which would respond to this signal, and expression appeared to persist for some time after the transformation (Figure 13G and 13H). This pattern of gene expression is unlike that described for any known molecule. Although the early endothelial expression pattern is similar to that characterized for the tyrosine kinases *tek* and *flk*-1 (Dumont et al., 1992, *Oncogene* 7:1471-1480; Millauer et al., 1993, *Cell* 72:835-846), there are striking differences at later stages which clearly indicate that *lacZ* expression in the transgenic animals marks a novel gene.

7.2.2. EXPRESSION ANALYSIS BY NORTHERN BLOT

Expression of *del-1* in various fetal and adult tissues was examined by Northern blot analysis (Tables 1 and 2). A portion of the mouse cDNA clone (0.3 kb Sac I probe) was used as a probe on six poly A RNA filters purchased from Clontech Inc. Human fetal tissues which were undergoing vasculogenesis were positive (Table 2). An organ blot generated with RNA from a 15.5 day mouse embryo indicated expression in highly vascular organs such as kidney, lung, nervous system and head. Also, the time course of expression in whole mouse embryos was consistent with the β-gal staining results observed in transgenic mice (Table 3). In general, adult mouse tissues were negative, or only weakly positive, (Table 4). Mouse cDNA clones isolated from a brain cDNA library appeared to be identical to the embryonic *del-1*. Two human cancer cell lines tested were weakly positive (Table 5). The results of Northern blot analysis were

basically consistent with the pattern for a gene which was specifically active during endothelial cell development.

Table 1

<u>Human Adult</u>

heart	+
brain	++++
placenta	-
lung	-
liver	-
spleen	-
thymus	-
prostate	-
testis	-
ovary	+
skeletal muscle	-
kidney	-
pancreas	-
small intestine	+
colon	-
peripheral blood leukocyte	+/-

Table 2

<u>Human Fetal</u>

brain	+++
lung	+++
liver	+
kidney	++
(Pooled from 17-26 wks)	

Table 3

Mouse Embryo

7-day	-
11-day	++
15-day	+++
17-day	++

Table 4

Mouse Adult

heart	-
brain	-
spleen	+
lung	-
liver	-
skeletal muscle	-
kidney	-

Table 5

Human Cancer Cell

Promyelocytic leukemia HL60	+/-
HeLa cell S3	+
chronic myelogenous leukemia K-562	-
lymphoblastic leukemia MOLT4	-
Burkit's lymphoma Raji	-
colorectal adenocarcinoma SW480	-
lung carcinoma A549	-
melanoma G361	-

7.2.3. EXPRESSION ANALYSIS BY RT-PCR

RNA from mouse yolk sac (day 8 through day 12) and mouse fetal liver (day 13 through day 18) were tested for *del-1* expression by RT-PCR. All tested samples were positive, consistent with the Northern blot analysis and results from β-gal staining in transgenic mice (Table 6). Several mouse yolk sac-derived cell lines were also tested by RT-PCR for expression of *del-1*. For comparison, several other cell lines and total d15 mouse fetal liver RNA samples were tested. All samples shown in Table 7 except ECV304 (a human endothelial cell line) were of mouse origin. The yolk sac-derived cell lines grown in long-term culture were not expressing *del-1* at a detectable level. These cell cultures were not forming endothelial cell-like structures under these conditions. In contrast, an endothelial tumor line, EOMA, expressed high levels of *del-1*.

Table 6

Yolk Sac and Fetal Liver

Sample	Result
d8 Yolk Sac	+
d9 Yolk Sac	+
d10 Yolk Sac	+
d11 Yolk Sac	+
d12 Yolk Sac	+
d13 Fetal Liver	+
d14 Fetal Liver	+
d15 Fetal Liver	+
d16 Fetal Liver	+
d17 Fetal Liver	+
d18 Fetal Liver	+

Table 7

Cell Lines

cell line	*del-1*
3T3 A31	-
Sto 1	++
YS4	-
Pro135	-
Pro175	-
D-1	-
A10	-
ROSA02	-
d15FL	++
EOMA	+++
ECV304 (human)	-

A number of human tumors implanted in nude mice and cultured *in vitro* were shown to express *del-1* by RT-PCR. For example, Table 8 shows the expression of *del-1* in human osteosarcoma cell line 143B *in vivo* and *in vitro*. EOMA was used as a positive control. CD34, *flk-1* and *tie-2* are known markers for endothelial cells. When human and mouse *del-1* specific PCR primers were used, both human (tumor) and murine (host) *del-1* expression was detected. In addition, a variety of human tumor cell lines expressed *del-1* in culture (Table 9). These results indicate that Del-1 may be used as a tumor marker in certain cancers diagnostically and therapeutically. In addition, host expression of *del-1* is also up-regulated, possibly due to angiogenesis in tumor sites.

Table 8

<u>Human osteosarcoma 143B</u>

Sample	Actin	*del-1*	CD34	*flk-1*	*tie-2*
control nude mouse skin	-	-	nd	nd	nd
7 day tumor	+	+	nd	nd	nd
10 day tumor	+	+	+	+	+
14 day tumor	+	+	+	+	+
cultured 143B cells	+	+	-	-	-
EOMA	+	+	+	+	+

nd = not determined

Table 9

<u>Human tumor cell lines</u>

Cell Type	Sample	27 cycles	33 cycles
Normal	Myoblast HYSE-E HYS-VS1	+ + ++	+++ +++ ++++
Leukemia	K562 HEL Mo7e	- - -	- +/- -
Glioblastoma	U-118 MG U-87 MG	+ ++	+++ +++
CNS Tumor	SF295 U251 SNB75 SNB19 SF539	+ ++ ++ + +	+++ ++++ ++++ +++ +++
Osteosarcoma	143B	+	++++
Breast Carcinoma	DU4475 MCF-7 MDA231	- +/- -	- +++ ++-
Endothelial	ECV304 HUVEC	- +	- +++

8. EXAMPLE: IMMUNOREACTIVITY OF DEL-1 GENE PRODUCT

8.1. MATERIALS AND METHODS

8.1.1. ANTIBODY PRODUCTION

A partial *del-1* cDNA encoding amino acids 353 to 489 of the murine gene was cloned into pMALC2 (New England Biolabs) to generate a maltose binding protein-partial Del-1 fusion protein. The *del-1* sequence included in this construct encodes a portion of the carboxyl terminal discoidin-like domain. Recombinant fusion protein was expressed and purified over an amylose affinity matrix according to the manufacturer's recommendations. Protein was emulsified into Freund's complete adjuvant, and injected as multiple subcutaneous injections into two New Zealand White rabbits. Boosting and harvesting of immune serum was performed according to established methodology (Harlow and Lane, 1988, Antibody: A Laboratory Manual, Cold Spring Harbor Laboratory). Immune serum obtained after the second boost was subjected to affinity purification. First, the antiserum was precleared over a Sepharose column coupled to total bacterial lysate. Subsequently, the antiserum was purified over an affinity column made from recombinant fusion protein coupled to Sepharose. The specificity of the antiserum was evaluated first with western blots containing proteins from bacteria expressing the recombinant fusion protein before and after cleavage with factor Xa, or the maltose binding protein alone. Whole bacterial lysates from cells induced with IPTG were run on polyacrylamide gels, transferred to nitrocellulose, and probed with the affinity-purified antiserum. While crude antiserum labeled bands corresponding to maltose binding protein and the Del-1 portion of the fusion protein, affinity-purified antiserum specifically labeled the Del-1 component of the fusion protein.

8.1.2. WESTERN BLOT

For western blots of eukaryotic proteins, cells were harvested by lysis in a standard lysis buffer or Laemmli loading buffer. Cell culture supernatant was collected and

concentrated by centrifugation in a centricon filter, and extracellular matrix harvested by first removing cells with 1 mM EDTA in PBS, and then scraping the cell culture dish with a small volume of Laemmli buffer at 90°C.

8.1.3. IMMUNOHISTOCHEMISTRY

Immunohistochemistry was performed on sections prepared from Bouin's fixed, paraffin-embedded, staged mouse embryos according to well established methodology (Hogan et al., 1994, *Manipulating the Mouse Embryo*, Cold Spring Harbor Press; Quertermous et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:7066). The affinity-purified Del-1 antiserum was employed at a dilution of 1:500 to 1:1000, and the specificity of staining verified by competition with recombinant protein. Staining of cartilage was amplified by pre-treating the section with dilute trypsin solution.

8.1.4. TRANSFECTION OF YOLK SAC CELLS

A eukaryotic expression vector was constructed by cloning the entire open reading frame of the major *del-1* transcript into phbAPr-3-neo (Gunning et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:4831). This construct was transfected into yolk sac cells with Lipofectamine (Gibco BRL), and clones selected in the presence of 1000 μg/ml of G418. Clones were evaluated for *del-1* expression by northern and western blotting, and a group of clones with varying amounts of Del-1 protein were selected for further study. To serve as negative controls, a group of clones were randomly selected from a transfection with the empty phbAPr-3-neo vector.

8.2. RESULTS

The major murine *del-1* coding sequence was inserted into a eukaryotic expression vector and transfected into Del-1-non-expressing yolk sac cells (Wei et al., 1995, Stem Cell 13:541). Pooled transfectants with an empty expression vector or the *del-1* construct were selected in G418.

Lysates, cell culture supernatants and extracellular matrix were prepared from transfected cells, and reacted with an affinity-purified rabbit antiserum in Western blots. The polyclonal antiserum was generated to recombinant Del-1 fusion protein expressed in bacteria. Figure 14A shows that a band of 52,000 daltons molecular weight was recognized in cell lysates prepared by harvesting the cells in lysis or standard Laemmli gel loading buffer, and in extracellular matrix. This band corresponds with the predicted molecular weight for Del-1 based on the deduced amino acid sequence, and represented the full-length Del-1 protein. In contrast, no protein was identified with culture supernatants harvested from the transfectants, even when concentrated 100-fold. Additionally, smaller proteolytic fragments were also detected. These results indicate that Del-1 is secreted across the surface of endothelial cells, and deposited in the extracellular matrix.

Several stably transfected yolk sac cell clones with the *del-1* gene were selected (Figure 14B). When the transfected cells were reacted with the aforementioned antibody, both the membrane of certain yolk sac cells and the extracellular matrix were stained as compared with mock-transfected yolk sac cells as negative control (Figure 15A, 15B). In keeping with this staining pattern, immunostaining of developing bone of a 13.5 day mouse embryo detected the Del-1 protein in the laquanae within the bone, which were composed of extracellular matrix proteins (Figure 16).

In order to test the expression of *del-1* in tumor cells by immunohistochemistry, human glioma cells were implanted in nude mice. The tumor was isolated, sectioned and stained with the aforementioned antibody followed by an anti-rabbit antibody conjugated with horse radish peroxidase and developed with Sigma Fast Red substitute. Figure 17A shows that the *in vivo* tumor cells were stained with the antibody in a polarized fashion. Polarization of *del-1* expression in tumor cells might have resulted from the interaction of the gene product with cellular receptors on adjacent cells. In

addition, a blood vessel of mouse origin traversing the human tumor was also stained with the antibody (Figure 17B).

9. EXAMPLE: DEL-1 INHIBITS VASCULAR FORMATION

9.1 MATERIALS AND METHODS

9.1.1. ANGIOGENESIS ASSAYS

In vitro angiogenesis assays on "MATRIGEL" (Biocoat, Becton Dickinson) were conducted in 24 well plates coated with 50 μl of "MATRIGEL". *del-1* transfectants and control transfectants were plated at a density of $5x10^4$ cells/well (low density) or $2x10^5$ cells/well (high density), and observed for seven days.

For the assay evaluating morphogenetic potential of wild type yolk sac cells on *del-1* conditioned matrix, the matrix was generated by growing 10^5 *del-1* transfectants in 6 cm dishes for 7 days. A control matrix was generated by growing control transfectants under identical conditions. Transfected cells were removed with 0.5 M EDTA and extensive washing, and 10^5 wild type yolk sac cells were plated on the matrix produced by the *del-1* or the control transfectants. Cells were cultured and observed for seven days.

For the *in vitro* angiogenesis sprouting assay, *del-1* and control transfectants were trypsinized, and 10^5 cells cultured in a 15 ml conical tubes for 48 hours. Cell cultures were then transferred into a bacterial petri dish, and cultured for 4-7 days. Under these conditions, cell aggregates were formed. Several aggregates were collected for *del-1* and control transfectants, and these were transferred to 24 well plates coated with "Matrigel". Sprouting angiogenesis was evaluated at 24 and 48 hours.

9.2. RESULTS

The yolk sac cell line, YS-B, was chosen as the parental cell for *del-1* transfection because it had characteristics of embryonic endothelial cells, did not express *del-1*, was clonal and long lived in culture (Figure 18A). Most importantly, these cells provided a model of vascularization

of the early yolk sac. While they were easily grown and maintained with frequent passage, when allowed to accumulate to high density they spontaneously formed vascular structures. This process was accelerated when the cells were plated on the basement membrane-like material "MATRIGEL", on which they behaved similar to various types of cultured endothelial cells (Figure 18B). Cell lines transfected with the cDNA encoding of the major form of *del-1* were selected for varying levels of expression of the transfected construct (Figure 14B). Cell lines transfected with the empty expression plasmid were selected to serve as negative controls.

The *del-1* transfected yolk sac clones and mock-transfected yolk sac lines were compared for their ability to form branching vascular-like structures on "MATRIGEL". After 24 hours on "MATRIGEL", the negative control transfectants had established an intricate network typical for these cells (Figure 18C). Cells (L10) expressing high levels of *del-1* showed a markedly different pattern, assembling into multiple well-spaced clusters (Figure 18D). This abrogation of morphogenesis was directly related to the level of *del-1* expression, as low *del-1* expressing clones, L13 and L14, showed some degree of branching morphology.

Since Del-1 protein is deposited in the extracellular matrix, one *del-1* expressing clone, L10, was used to generate a cell culture matrix containing Del-1 protein. Matrix generated by negative control clones should differ only by the absence of Del-1. Transfected and control lines were cultured for 7 days, and then gently removed from the culture dish by extensive washing with 1 mM EDTA. By visual inspection, only a rare cell was not removed with this technique. Non-transfected native yolk sac cells were then plated on the Del-1-containing and the control matrices, and scored for their ability to assemble into a network. The yolk sac cells required several days at high density to undergo morphogenesis, and the network was lace-like in appearance. Cells grown on the matrix produced by negative

control transfectants were able to produce the network (Figure 18E). In contrast, yolk sac cells grown on matrix containing Del-1 revealed no evidence of morphogenesis. They formed instead a dense monolayer (Figure 18F).

Next, an *in vitro* angiogenesis sprouting assay was employed with the transfected yolk sac lines. This assay has been employed to evaluate angiogenic potential (Pepper at al. 1991, J. Cell. Physiol. 146:170). Transfected cells were allowed to stand overnight in a conical tube to allow them to aggregate, and the cell mass was then placed on "MATRIGEL". The ability of the *del-1* expressing cells to migrate onto the "MATRIGEL" and assemble into branching structures was compared to control cells. Within 24 hours, the control cells formed a series of branching projections, while the cells expressing *del-1* remained virtually confined to the cellular aggregate (Figure 18G and 18H). While there was some evidence of spreading of the *del-1* expressing cells after 48 hours, it was more as a sheet rather than a sprouting structure.

Hence, Del-1 inhibits vascular morphogenesis and may be used to regulate endothelial cell differentiation.

10. EXAMPLE: DEL-1 BINDS TO INTEGRIN ALPHA V BETA 3

10.1. MATERIALS AND METHODS

10.1.1. RECOMBINANT DEL-1 PURIFICATION AND REFOLDING

Recombinant murine Del-1 protein (major form) was prepared using an *E. coli* expression system and protein refolding technique. *E. coli* cells with the *del-1* containing pET28a vector (Novagen Inc.) were grown and induced following the protocol recommended by the manufacturer. Approximately 50 to 100 mg of crude recombinant Del-1 were routinely produced from 1L of bacterial culture in the form of insoluble cytoplasmic inclusion bodies. Inclusion bodies were isolated by sonication of the *E. coli* cells, centrifugation and collection of the pellet fraction.

Inclusion bodies from 500 ml of culture were then washed three times with 50 ml of 2M Urea, 0.025 M Tris-Cl (pH8.0), 0.025% Triton X100. This procedure yielded a crude, insoluble, Del-1 product of > 80% purity.

Recombinant Del-1 was dissolved by suspending the pellet from 500 ml of culture in 2.5 ml of 8M Urea, 100 mM DTT, 0.1 M Tris-Cl (pH8.0), 0.05% Triton X100, followed by incubation at room temperature for 1 hr. Insoluble material remaining was removed by centrifugation and the soluble supernatant fraction was diluted 10 fold to 25 ml with 8M Urea, 100 mM Tris-Cl (pH 8.0), 0.05% Triton X100. Protein concentration was then measured by Bradford protein determination assay.

Soluble, reduced Del-1 was refolded by diluting to a final concentration of 0.01 mg/ml into refolding buffer: 100 mM Tris-Cl (pH8.0), 100 mM $(NH_4)_2SO_4$, 2 mM reduced glutathione, 0.5 mM oxidized glutathione, 0.05% sodium azide, 0.025 mg/ml PMSF. Refolding was performed by incubating this reaction mix at 4°C for one week. Refolded Del-1 was then concentrated using an Amicon spiral concentrator and the soluble material remaining was collected.

The recombinant Del-1 product produced from the pET28a expression vector is a fusion protein with both N-terminal and C-terminal polyhistidine tags. This product was purified using the Novagen His tag resin purification system, following the protocol recommended by the supplier.

Refolded murine recombinant Del-1 was soluble and stable when stored at 4°C in Tris-Cl buffer with 100 mM $(NH_4)_2SO_4$ at concentrations of less than or equal to 100 mg/ml.

10.1.2. CELL ADHESION ASSAYS

Human umbilical vein endothelial cells (HUVEC) (Clonetics Inc., San Diego, CA) were grown as indicated by the supplier in endothelial growth media supplemented with 10 ng/ml human recombinant epidermal growth factor, 1 μg/ml hydrocortisone, 50 μg/ml gentamicin, 12 μg/ml bovine brain extract and 2% FBS. Cells were grown at 37°C/5% CO_2 to 70% confluency before use in the binding assay. Non-tissue

culture treated 96 well plates were coated with appropriate levels of target protein (1-20 μg of either murine recombinant Del-1, vitronectin, or BSA) diluted in calcium and magnesium free PBS for 24 hrs at 4°C. The plates were washed with PBS and blocked for 30 min with a solution of heat treated (95°C for 5 min) PBS containing 3% BSA. HUVEC cells were harvested by trypsinization and resuspended in an adhesion buffer (Hanks balanced salt solution pH 7.4 containing 10mM Hepes, 2.2 mM $MgCl_2$, 2 mM $Cacl_2$, 0.2mM $MnCl_2$ and 1% BSA). Cells (10^4/100 μl) were added to each well in the presence or absence of the indicated antagonists or controls at varying concentrations. Antagonists included anti-human αVβ3 (clone LM609, Chemicon Inc.), RGE peptides (the inactive control GRGESP) or RGD the stable antagonist GPenGRGDSPCA or GRGDdSP all from Gibco). Cells were incubated at 37°C/5% CO_2 for 60-90 min and wells were washed until no cells remained in the BSA control. To count remaining cells, 100 μl of endothelial media was added to each well. Cells number was determined by the Promega Cell titer AQ as indicated by the manufacturer.

10.2. RESULTS

Recombinant Del-1 protein and *del-1* transfectants bound HUVEC. In order to identify a cellular receptor on HUVEC for Del-1, various peptides and antibodies were used to inhibit the interactions between Del-1 and HUVEC in cell adhesion assays. Figure 19 shows that an anti-αVβ3 antibody specifically inhibited recombinant Del-1 binding to HUVEC. In contrast, anti-αVβ5 did not inhibit, nor did the control Ig. Furthermore, an RGD peptide was also shown to inhibit Del-1 binding to HUVEC (Figure 20). Similar results were obtained using extracellular matrix obtained from *del-1* transfected cells. Therefore, Del-1 binds to αVβ3 expressed by HUVEC, possibly via RGD in its second EGF-like domain.

αVβ3 is an integrin expressed by certain cell types and is associated with bFGF-induced angiogenic endothelial cells. Agents that bind to this integrin induce apoptosis of

angiogenic endothelial cells. Since Del-1 binds to this integrin, it may be used to induce apoptosis during angiogenesis in tumor sites to reduce tumor growth.

11. EXAMPLE: CHROMOSOMAL LOCALIZATION OF HUMAN *DEL-1*

DNA from P1 clone 10043 was labeled with digoxigenin dUTP by nick translation. The labeled probe was combined with sheared human DNA and hybridized to normal metaphase chromosomes derived from PHA stimulated peripheral blood lymphocytes in a solution containing 50% formamide, 10% dextran sulfate and 2X SSC. Specific hybridization signals were detected by incubating the hybridized slides in fluoresceinated antidigoxigenin antibodies followed by counterstaining with DAPI. The initial experiment resulted in specific labeling of the long arm of a group B chromosome.

A second experiment was conducted in which a probe that had previously been mapped to 5q34, and confirmed by cohybridization with a probe from the cri du chat locus which is known to localize to 5p15, was cohybridized with clone 10043. This experiment resulted in the specific labeling of the mid and distal long arm of chromosome 5 (Figure 21 A and B). Measurements of 10 specifically hybridized chromosomes 5 demonstrated that clone 10043 was located at a position which was 29% of the distance form the centromere to the telomere of chromosome arm 5q, an area that corresponded to band 5q14. A total of 80 metaphase cells were analyzed with 74 exhibiting specific labeling. This region of the chromosome has been found to be a break point in some human cancers (Wieland and Bohm, 1994, *Cancer Res.* 54:1772; Fong et al., 1995, *Cancer Res.* 55:220; Wieland et al., 1996, 12:97, *Oncogene* 12:97). Thus, chromosome 5 aberrations may lead to altered expression of *del-1* and contribute to the malignant phenotype.

12. DEPOSIT OF MICROORGANISMS

The following organisms were deposited with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852.

Strain Designation	Accession No.
Hu DEL-1.Z1	ATCC 97155
Hu DEL-1.Z20	ATCC 97154
mus DEL-1.1	ATCC 97196
mus DEL-1.18	ATCC 97197

The present invention is not to be limited in scope by the exemplified embodiments or deposited organisms which are intended as illustrations of single aspects of the invention, and any clones, DNA or amino acid sequences which are functionally equivalent are within the scope of the invention. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims. It is also to be understood that all base pair sizes given for nucleotides are approximate and are used for purposes of description.

All publications cited herein are incorporated by reference in their entirety.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.

(ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-034

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864/9741
(C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1               5                   10                  15
```

```
Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
            20                  25                  30

Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
        35                  40                  45

Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
    50                  55                  60

Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
65                  70                  75                  80

Leu Pro Leu Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
1               5                   10                  15

Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
            20                  25                  30

Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
        35                  40                  45

Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
    50                  55                  60

Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
65                  70                  75                  80

Leu Pro Val Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
1   5   10   15

Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
            20   25   30

His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
        35   40   45

Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
    50   55   60

Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
65   70   75   80

Ile Pro Lys Xaa Xaa
                85

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1   5   10   15

Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
            20   25   30

Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
        35   40   45

Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
    50   55   60

Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Xaa
                85

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1   5   10   15

Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
            20   25   30

Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
        35   40   45

Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
    50   55   60

Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65   70   75   80

Arg Pro Val Thr Trp
                85

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1   5   10   15

Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
            20   25   30

Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
        35   40   45

Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
    50   55   60

Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65   70   75   80

Ile Pro Xaa Xaa Xaa
                85

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1               5                   10                  15

Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
            20                  25                  30

Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
        35                  40                  45

Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
    50                  55                  60

Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65                  70                  75                  80

His Pro Leu Thr Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Asp Leu Xaa Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1               5                   10                  15

Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
            20                  25                  30

Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35                  40                  45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
    50                  55                  60

Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65                  70                  75                  80

Xaa Pro Xaa Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA      60

TTCCCAGTGG CCTTGATATT TAAACTGATT CCTGCCACCA GGTCCTTGGG CCACCCTGTC     120

CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCGCTCC TGGCCTCAGG     180

CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCG     240

CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGCGTGCGCG CACGGAAATC     300

GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC     360

AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG     420

TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTG     480

AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG     540

TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCCGGACCA GCCCAGGTCA     600

CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT       651
                    Met Lys His Leu Val Ala Ala Trp Leu Leu Val
                     1               5                  10

GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC       699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn
            15                  20                  25

CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT       747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp
        30                  35                  40

GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC       795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys
    45                  50                  55

TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA       843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala
 60                  65                  70                  75

GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA       891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile
                80                  85                  90

AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT       939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys
            95                 100                 105

CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT       987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys
        110                 115                 120

GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT      1035
```

```
Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala
    125                 130                 135

AAC TAC TCT TGT GAA TGC CCA GGA GAA TTT ATG GGA CGA AAT TGT CAA         1083
Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln
140                 145                 150                 155

TAT AAA TGC TCT GGG CAC TTG GGA ATC GAA GGT GGG ATC ATA TCT AAT         1131
Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn
                160                 165                 170

CAG CAA ATC ACA GCT TCA TCT AAT CAC CGA GCT CTT TTT GGA CTC CAG         1179
Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln
            175                 180                 185

AAG TGG TAT CCC TAC TAT GCT CGA CTT AAT AAG AAG GGC CTT ATA AAT         1227
Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn
        190                 195                 200

GCC TGG ACA GCT GCT GAA AAT GAC AGA TGG CCA TGG ATT CAG ATA AAT         1275
Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn
    205                 210                 215

TTG CAA AGA AAA ATG AGA GTC ACT GGT GTT ATT ACC CAA GGA GCA AAA         1323
Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
220                 225                 230                 235

AGG ATT GGA AGC CCA GAG TAC ATA AAA TCC TAC AAA ATT GCC TAC AGC         1371
Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser
                240                 245                 250

AAT GAC GGG AAG ACC TGG GCA ATG TAC AAA GTA AAA GGC ACC AAT GAA         1419
Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
            255                 260                 265

GAG ATG GTC TTT CGT GGA AAT GTT GAT AAC AAC ACA CCA TAT GCT AAT         1467
Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn
        270                 275                 280

TCT TTC ACA CCC CCA ATC AAA GCT CAG TAT GTA AGA CTC TAC CCC CAA         1515
Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
    285                 290                 295

ATT TGT CGA AGG CAT TGT ACT TTA AGA ATG GAA CTT CTT GGC TGT GAG         1563
Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
300                 305                 310                 315

CTC TCA GGC TGT TCA GAA CCT TTG GGG ATG AAA TCA GGG CAT ATA CAA         1611
Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
                320                 325                 330

GAC TAC CAG ATC ACT GCC TCC AGC GTC TTC AGA ACA CTC AAC ATG GAC         1659
Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp
            335                 340                 345

ATG TTT ACT TGG GAA CCA AGG AAA GCC AGG CTG GAC AAG CAA GGC AAA         1707
Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
        350                 355                 360

GTA AAT GCC TGG ACT TCC GGC CAT AAC GAC CAG TCA CAA TGG TTA CAG         1755
Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
    365                 370                 375
```

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA 1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
380 385 390 395

GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT 1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
400 405 410

TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG 1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln
415 420 425

AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG 1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
430 435 440

AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT 1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu
445 450 455

CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC 2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly
460 465 470 475

TGC GCA GAG GAG GAA TGAAGTGCGG GGCCGCACAT CCCACAATGC TTTTCTTTAT 2098
Cys Ala Glu Glu Glu
480

TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAAACT GCATTTGTTT 2158

TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG 2218

CCTTTTTAAT AATTTAATTT GGTTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT 2278

CTGTGAGTTA CTCTTCTTGT TCTCT 2303

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115 120 125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
210 215 220

Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
225 230 235 240

Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
245 250 255

Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
260 265 270

Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
275 280 285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
290 295 300

Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
305 310 315 320

Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
325 330 335

Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
340 345 350

Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
355 360 365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
370 375 380

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
385 390 395 400

His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
405 410 415

```
Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
            420                 425                 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
        435                 440                 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
    450                 455                 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465                 470                 475                 480
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG        48
Ser Leu  *  Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
  1               5                  10                  15

CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT        96
Arg  *  Gly Lys Arg Thr Ser Ser  *  Ile Leu  *   *  Gly Arg Ser
            20                  25                  30

CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG       144
Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr
        35                  40                  45

ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC       192
Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg
    50                  55                  60

TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG       240
Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln
 65                  70                  75                  80

TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT       288
Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly
                 85                  90                  95

ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA       336
Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro
            100                 105                 110

GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA       384
Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser
        115                 120                 125
```

```
GAT GAA GAA GAA CCA ACT TCA GCA GGT CCC TGC ACT CCT AAT CCA TGC        432
Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro Asn Pro Cys
    130                 135                 140

CAT AAT GGA GGA ACC TGT GAA ATA AGT GAA GCA TAC CGA GGG GAT ACA        480
His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg Gly Asp Thr
145                 150                 155                 160

TTC ATA GGC TAT GTT TGT AAA TGT CCC CGA GGA TTT AAT GGG ATT CAC        528
Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn Gly Ile His
                165                 170                 175

TGT CAG CAC AAC ATA AAT GAA TGC GAA GTT GAG CCT TGC AAA AAT GGT        576
Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys Lys Asn Gly
            180                 185                 190

GGA ATA TGT ACA GAT CTT GTT GCT AAC TAT TCC TGT GAG TGC CCA GGC        624
Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu Cys Pro Gly
        195                 200                 205

GAA TTT ATG GGA AGA AAT TGT CAA TAC AAA TGC TCA GGC CCA CTG GGA        672
Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly Pro Leu Gly
    210                 215                 220

ATT GAA GGT GGA ATT ATA TCA AAC CAG CAA ATC ACA GCT TCC TCT ACT        720
Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala Ser Ser Thr
225                 230                 235                 240

CAC CGA GCT CTT TTT GGA CTC CAA AAA TGG TAT CCC TAC TAT GCA CGT        768
His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr Tyr Ala Arg
                245                 250                 255

CTT AAT AAG AAG GGG CTT ATA AAT GCG TGG ACA GCT GCA GAA AAT GAC        816
Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala Glu Asn Asp
            260                 265                 270

AGA TGG AAG CGG TGG ATT CAG ATA AAT TTG CAA AGA AAA ATG AGA GTT        864
Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys Met Arg Val
        275                 280                 285

ACT GGT GTG ATT ACC CAA GGG GCC AAG AGG ATT GGA AGC CCA GAG TAT        912
Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro Glu Tyr
    290                 295                 300

ATA AAA TTC TAC AAA ATT GCC TAC AGT AAT GAT GGA AAG ACT TGG GCA        960
Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr Trp Ala
305                 310                 315                 320

ATG TAC AAA GTG AAA GGC ACC AAT GAA GAC ATG GTG TTT CGT GGA AAC       1008
Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg Gly Asn
                325                 330                 335

ATT GAT AAC AAC ACT CCA TAT GCT AAC TCT TTC ACA CCC CCC ATA AAA       1056
Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro Ile Lys
            340                 345                 350

GCT CAG TAT GTA AGA CTC TAT CCC CAA GTT TGT CGA AGA CAT TGC ACT       1104
Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His Cys Thr
        355                 360                 365

TTG CGA ATG GAA CTT CTT GGC TGT GAA CTG TCG GGT TGT TCT GAG CCT       1152
Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser Glu Pro
    370                 375                 380
```

```
CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG ATC ACT GCC TCC      1200
Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser
385                 390                 395                 400

AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA CCA AGG      1248
Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg
                405                 410                 415

AAA GCT CGG CTG GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC      1296
Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly
            420                 425                 430

CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC      1344
His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr
        435                 440                 445

AAA GTG ACT GGC ATC ATT ACA CAA GGA GCT AAA GAT TTT GGT CAT GTA      1392
Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val
    450                 455                 460

CAG TTT GTT GGC TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC      1440
Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His
465                 470                 475                 480

TGG ACT GTA TAC CAG GAT GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG      1488
Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln
                485                 490                 495

GGA AAT TTT GAC AAT GAC ACT CAC AGA AAA AAT GTC ATC GAC CCT CCC      1536
Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro
            500                 505                 510

ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT TGG TCC TGG TAC GGG AGG      1584
Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg
        515                 520                 525

ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG GAG GAA TGA GGG      1632
Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu  *  Gly
    530                 535                 540

GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT ATC TCC      1680
Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser
545                 550                 555                 560

ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT      1728
Met Glu  *  Thr Val  *  Asn Leu  *  Glu Thr Glu Trp Phe Phe Phe
                565                 570                 575

TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT      1776
Phe Ser  *  Lys Ser Gly Gln Ile Met Val Gly Asn  *  Arg Cys Phe
            580                 585                 590

TAC C                                                                1780
Tyr
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ser Leu  *  Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
  1             5                   10                  15

Arg
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Gly Lys Arg Thr Ser Ser
  1             5
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 517 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Ile Leu  *   *  Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser
1               5                   10                  15

Ala Thr Leu Pro Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro
            20                  25                  30

Gly Asp Gly Ile Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly
        35                  40                  45

Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro
    50                  55                  60

Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly
65                  70                  75                  80

Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser
                85                  90                  95

Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly
            100                 105                 110

Pro Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser
        115                 120                 125

Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro
    130                 135                 140

Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu
145                 150                 155                 160
```

```
Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn
                165                 170                 175

Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr
            180                 185                 190

Lys Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln
        195                 200                 205

Gln Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys
    210                 215                 220

Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala
225                 230                 235                 240

Trp Thr Ala Ala Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn
                245                 250                 255

Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
            260                 265                 270

Arg Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser
        275                 280                 285

Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
    290                 295                 300

Asp Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn
305                 310                 315                 320

Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
                325                 330                 335

Val Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
            340                 345                 350

Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
        355                 360                 365

Asp Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp
    370                 375                 380

Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
385                 390                 398                 400

Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
                405                 410                 415

Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
            420                 425                 430

Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
        435                 440                 445

Tyr Ser Asn Asp Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln
    450                 455                 460

Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
465                 470                 475                 480

Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu
                485                 490                 495
```

Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly
500 505 510

Cys Thr Glu Glu Glu
515

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
1 5 10 15

Ser Met Glu * Thr Val * Asn Leu
20 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTTATT    60
ACCCAAGGAG CAAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC   120
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC   180
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA   240
GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA   300
CTTCTTGGCT GTGAGCTC                                                 318
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1               5                   10                  15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
            20                  25                  30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
        35                  40                  45

His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
    50                  55                  60

Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
65                  70                  75                  80

Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu
                85                  90                  95
```

Asp Gly Xaa Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp
            100   105   110

Lys Glu Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met
        115   120   125

Phe Asn Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser
    130   135   140

Cys His Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu
145   150   155   160

His Gly Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp
                165   170   175

Ser Gln Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala
            180   185   190

Phe Gly Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Lys Ile
        195   200   205

Asn Ala Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val
    210   215   220

Asp Leu Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala
225   230   235   240

Arg Asp Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His
                245   250   255

Ser Asp Asp Gly Val Gln Trp Thr Val Tyr Xaa Xaa Glu Glu Gln Gly
            260   265   270

Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys
        275   280   285

Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
    290   295   300

Val Ser Trp His Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
305   310   315   320

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
1   5   10   15

Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp
            20   25   30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
50 55 60

Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
65 70 75 80

Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
85 90 95

Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
100 105 110

Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
115 120 125

Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
130 135 140

Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
145 150 155 160

Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
165 170 175

Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
180 185 190

Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
195 200 205

Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
210 215 220

Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
225 230 235 240

Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
245 250 255

Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
260 265 270

Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
275 280 285

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
290 295 300

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
305 310 315 320

Thr

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1               5                   10                  15

Val Pro Gln Phe Gly Lys Gly Asp Ile
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1               5                   10                  15

Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
            20                  25                  30

Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
        35                  40                  45

Glu Glu Glu Pro Thr Ser Ala Gly Pro
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1               5                   10                  15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
            20                  25                  30
```

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
20 25 30

Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT 60

GTAGGTTCCT TTTCCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACTG TTCTAGTGTT 120

GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT 180

GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT 240

GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA 300

ATATGTACAG 310

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 549..1211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGGG CCAAAGCCAG CTAGGCTCAG 60

TCTCACACGC GCGCCGCCAC TGTTTGTATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC 120

CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC 180

GTGAGCCGTA GTCACTGCTG GCCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA 240

GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC 300

CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA 360

ATCACCCTTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCCAAGATTT GAGAAGCGCT 420

GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG 480

CGCGCCTCGC CTACTGTGCC CTCCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA 540

GAAGGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGACTCAG CCTCGGGGTG 600

CCCCAGTTCG GCAAAGGTGA CATTTGCAAC CCGAACCCCT GTGAAAATGG TGGCATCTGT 660

CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGTC CAGAAGGCTT CGCAGGTCCG 720

AACTGCTCTA GTGTTGTGGA GGTTGCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC 780

TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA 840

GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG 900

CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT 960

GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA 1020

TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA 1080

TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT 1140

AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTCAG 1200

GTAACAGTGG GATGAGACAA ATCCATTTCC CAAATTATCA GAATCATTAT AGAAGTAGGT 1260

TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTTAAAATG TGATTTAGTT CAGAATTAAC 1320

ATGGTTGGAA ACTCTAAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA 1380

ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG 1440

AAAAAGATCT TATCATTTCA TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA 1500

TAAATACCTA ATTGAAAAAA GTTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTCAGAG 1560

ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTTGTGAGA AATAGTTTCC CATGTGCAAA 1620

TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA 1680

TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTACTACAGA 1740

AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA 1800

TAGCCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAAGCAG AAATGAGATG 1860

TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT 1920

CTTTAAGATA GTCACTAACA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG 1980

TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAAG TTTTGAAATA 2040

AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAATCAAC 2100

AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG 2160

GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG 2220

TGCCACATTT TGTTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC 2280

ACTATAATTT GAATAAAAGC CGGAATTC 2308

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

```
Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
            20                  25                  30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
        35                  40                  45

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
    50                  55                  60

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
65                  70                  75                  80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
                85                  90                  95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
            100                 105                 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
        115                 120                 125

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
    130                 135                 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145                 150                 155                 160

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
                165                 170                 175

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
            180                 185                 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
        195                 200                 205

Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
    210                 215                 220

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
225                 230                 235                 240

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
                245                 250                 255

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
            260                 265                 270

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
        275                 280                 285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
    290                 295                 300

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
305                 310                 315                 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
                325                 330                 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
            340                 345                 350
```

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
        355   360   365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu
    370   375   380

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa
385   390   395   400

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
                405   410   415

Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys
            420   425   430

Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
        435   440   445

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
    450   455   460

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
465   470   475

Glu
480

WHAT IS CLAIMED IS:

1. An isolated nucleotide nucleic acid molecule comprising a nucleotide sequence encoding protein which has three EGF-like domains and two discoidin I/factor VIII-like domains.

2. An isolated nucleic acid molecule, comprising a nucleotide sequence that hybridizes under stringent conditions to a nucleic acid molecule having the nucleotide sequence of SEQ ID NO: 19.

3. An isolated nucleic acid molecule, comprising a nucleotide sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO: 10 or its complement.

4. An isolated nucleic acid molecule, comprising a nucleotide sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO: 29 or its complement.

5. An isolated nucleic acid molecule, comprising a nucleotide sequence of SEQ ID NO: 28 or its complement.

6. A recombinant DNA vector containing a nucleotide sequence of Claim 2, 3, 4 or 5.

7. A recombinant DNA vector containing a nucleotide sequence that encodes a Del-1 fusion protein.

8. The recombinant DNA vector of Claim 6 in which the *del-1* nucleotide sequence is operatively associated with a regulatory sequence that controls gene expression in a host cell.

9. The recombinant DNA vector of Claim 7 in which the *del-1* fusion protein nucleotide sequence is operatively

associated with a regulatory sequence that controls fusion protein gene expression in a host cell.

10. An engineered host cell that contains the recombinant DNA expression vector of Claim 8.

11. An engineered cell line that contains the recombinant DNA expression vector of Claim 8 and expresses Del-1.

12. An engineered cell line that contains the recombinant DNA expression vector of Claim 9 and expresses Del-1 fusion protein.

13. The engineered cell line of Claim 11 or 12 which expresses the Del-1 on the surface of the cell.

14. The engineered cell line of Claim 11 or 12 that expresses the Del-1 as a soluble protein or fragments thereof.

15. A method for producing recombinant Del-1 comprising:

(a) culturing a host cell transformed with a recombinant DNA expression vector containing a nucleotide sequence that encodes a Del-1 protein; and

(b) recovering the Del-1 protein gene product from the cell culture.

16. A method for producing recombinant Del-1 fusion protein, comprising:

(a) culturing a host cell transformed with a recombinant DNA expression vector containing a nucleotide sequence that encodes a Del-1 fusion protein; and

(b) recovering the Del-1 fusion protein from the cell culture.

17. An isolated recombinant Del-1 protein which has three EGF-like domains and two discoidin I/factor VIII-like domains..

18. A fusion protein comprising Del-1 linked to a heterologous protein or peptide sequence or portions thereof.

19. An oligonucleotide which encodes an antisense sequence complementary to the *del-1* nucleotide sequence, and which inhibits translation of the *del-1* gene in a cell.

20. The oligonucleotide of Claim 19 which is complementary to a nucleotide sequence encoding the amino terminal region of the *del-1*.

21. An antibody which immunospecifically binds to an epitope of the Del-1.

22. The antibody of Claim 21 which is of monoclonal origin.

23. The antibody of Claim 22 which competitively inhibits the binding of a molecule to the Del-1.

24. The antibody of Claim 22 which is linked to a cytotoxic agent.

25. The antibody of Claim 22 which is linked to a radioisotope.

26. The antibody of Claim 22 which is anchored on a solid support.

27. The antibody of Claim 22 which is linked to biotin.

28. A method for screening and identifying antagonists of Del-1 comprising:

(a) contacting a cell line that expresses Del-1 with a test compound; and

(b) determining whether the test compound inhibits the expression or function of Del-1.

29. The method according to Claim 28 in which the cell line is a genetically engineered cell line.

30. The method according to Claim 28 in which the cell line endogenously expresses Del-1.

31. A method for screening and identifying a binding partner of Del-1 activity comprising:

(a) contacting Del-1 protein with a random peptide library such that Del-1 will recognize and bind to one or more peptide species within the library;

(b) isolating the Del-1 combination; and

(c) determining the sequence of the peptide isolated in step b.

32. The method according to Claim 31 in which the Del-1 protein is genetically engineered.

33. A method of detecting and isolating embryonic cells comprising incubating a cell mixture with an anti-Del-1 antibody, and isolating the antibody-bound cells.

ABSTRACT

The present invention relates to a member of a novel gene family referred to as developmentally-regulated endothelial cell locus-1 (*del-1*). In particular, the invention relates to *del-1* nucleotide sequences, Del-1 amino acid sequences, methods of expressing a functional gene product, and methods of using the gene and gene product. Since *del-1* is expressed in endothelial cells and certain cancer cells, it may be useful as an endothelial cell and tumor marker. In addition, the ability of Del-1 to inhibit vascular formation allows its use as an anti-angiogenic agent.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.

(ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/659,235
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-0034-999

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864/9741
(C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1               5                   10                  15
```

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
20 25 30

Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
35 40 45

Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
50 55 60

Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
65 70 75 80

Leu Pro Leu Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
20 25 30

Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
35 40 45

Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
50 55 60

Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
65 70 75 80

Leu Pro Val Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
1               5                   10                  15

Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
            20                  25                  30

His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
        35                  40                  45

Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
    50                  55                  60

Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
65                  70                  75                  80

Ile Pro Lys Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1               5                   10                  15

Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
            20                  25                  30

Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
        35                  40                  45

Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
    50                  55                  60

Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
65                  70                  75                  80

Xaa Xaa Xaa Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1               5                   10                  15

Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
            20                  25                  30

Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
        35                  40                  45

Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
    50                  55                  60

Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65                  70                  75                  80

Arg Pro Val Thr Trp
                85
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1               5                   10                  15

Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
            20                  25                  30

Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
        35                  40                  45

Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
    50                  55                  60

Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65                  70                  75                  80

Ile Pro Xaa Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1               5                   10                  15

Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
            20                  25                  30

Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
        35                  40                  45

Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
    50                  55                  60

Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65                  70                  75                  80

His Pro Leu Thr Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Asp Leu Xaa Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1               5                   10                  15

Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
            20                  25                  30

Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35                  40                  45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
    50                  55                  60

Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65                  70                  75                  80

Xaa Pro Xaa Xaa Xaa
                85
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA      60

TTCCCAGTGG CCTTGATATT TAAACTGATT CCTGCCACCA GGTCCTTGGG CCACCCTGTC     120

CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCGCTCC TGGCCTCAGG     180

CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCG     240

CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGCGTGCGCG CACGGAAATC     300

GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC     360

AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG     420

TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTG     480

AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG     540

TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCCGGACCA GCCCAGGTCA     600

CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT       651
                    Met Lys His Leu Val Ala Ala Trp Leu Leu Val
                      1               5                  10

GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC       699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn
            15                  20                  25

CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT       747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp
        30                  35                  40

GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC       795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys
    45                  50                  55

TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA       843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala
60                  65                  70                  75

GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA       891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile
                80                  85                  90

AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT       939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys
            95                 100                 105

CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT       987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys
        110                 115                 120

GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT      1035
```

```
Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala
    125                 130                 135

AAC TAC TCT TGT GAA TGC CCA GGA GAA TTT ATG GGA CGA AAT TGT CAA      1083
Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln
140                 145                 150                 155

TAT AAA TGC TCT GGG CAC TTG GGA ATC GAA GGT GGG ATC ATA TCT AAT      1131
Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn
                160                 165                 170

CAG CAA ATC ACA GCT TCA TCT AAT CAC CGA GCT CTT TTT GGA CTC CAG      1179
Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln
            175                 180                 185

AAG TGG TAT CCC TAC TAT GCT CGA CTT AAT AAG AAG GGC CTT ATA AAT      1227
Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn
        190                 195                 200

GCC TGG ACA GCT GCT GAA AAT GAC AGA TGG CCA TGG ATT CAG ATA AAT      1275
Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn
    205                 210                 215

TTG CAA AGA AAA ATG AGA GTC ACT GGT GTT ATT ACC CAA GGA GCA AAA      1323
Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
220                 225                 230                 235

AGG ATT GGA AGC CCA GAG TAC ATA AAA TCC TAC AAA ATT GCC TAC AGC      1371
Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser
                240                 245                 250

AAT GAC GGG AAG ACC TGG GCA ATG TAC AAA GTA AAA GGC ACC AAT GAA      1419
Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
            255                 260                 265

GAG ATG GTC TTT CGT GGA AAT GTT GAT AAC AAC ACA CCA TAT GCT AAT      1467
Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn
        270                 275                 280

TCT TTC ACA CCC CCA ATC AAA GCT CAG TAT GTA AGA CTC TAC CCC CAA      1515
Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
    285                 290                 295

ATT TGT CGA AGG CAT TGT ACT TTA AGA ATG GAA CTT CTT GGC TGT GAG      1563
Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
300                 305                 310                 315

CTC TCA GGC TGT TCA GAA CCT TTG GGG ATG AAA TCA GGG CAT ATA CAA      1611
Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
                320                 325                 330

GAC TAC CAG ATC ACT GCC TCC AGC GTC TTC AGA ACA CTC AAC ATG GAC      1659
Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp
            335                 340                 345

ATG TTT ACT TGG GAA CCA AGG AAA GCC AGG CTG GAC AAG CAA GGC AAA      1707
Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
        350                 355                 360

GTA AAT GCC TGG ACT TCC GGC CAT AAC GAC CAG TCA CAA TGG TTA CAG      1755
Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
    365                 370                 375
```

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA 1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
380 385 390 395

GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT 1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
400 405 410

TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG 1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln
415 420 425

AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG 1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
430 435 440

AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT 1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu
445 450 455

CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC 2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly
460 465 470 475

TGC GCA GAG GAG GAA TGAAGTGCGG GGCCGCACAT CCCACAATGC TTTTCTTTAT 2098
Cys Ala Glu Glu Glu
480

TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAAACT GCATTTGTTT 2158

TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG 2218

CCTTTTTAAT AATTTAATTT GGTTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT 2278

CTGTGAGTTA CTCTTCTTGT TCTCT 2303

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
                85   90   95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
            100   105   110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
        115   120   125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
    130   135   140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145   150   155   160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
                165   170   175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
            180   185   190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
        195   200   205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
    210   215   220

Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
225   230   235   240

Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
                245   250   255

Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
            260   265   270

Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
        275   280   285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
    290   295   300

Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
305   310   315   320

Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
                325   330   335

Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
            340   345   350

Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
        355   360   365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
    370   375   380

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
385   390   395   400

His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
                405   410   415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG 48
Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
1 5 10 15

CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT 96
Arg * Gly Lys Arg Thr Ser Ser * Ile Leu * * Gly Arg Ser
20 25 30

CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG 144
Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr
35 40 45

ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC 192
Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg
50 55 60

TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG 240
Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln
65 70 75 80

TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT 288
Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly
85 90 95

ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA 336
Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro
100 105 110

GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA 384
Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser
115 120 125

```
GAT GAA GAA GAA CCA ACT TCA GCA GGT CCC TGC ACT CCT AAT CCA TGC         432
Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro Asn Pro Cys
    130                 135                 140

CAT AAT GGA GGA ACC TGT GAA ATA AGT GAA GCA TAC CGA GGG GAT ACA         480
His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg Gly Asp Thr
145                 150                 155                 160

TTC ATA GGC TAT GTT TGT AAA TGT CCC CGA GGA TTT AAT GGG ATT CAC         528
Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn Gly Ile His
                165                 170                 175

TGT CAG CAC AAC ATA AAT GAA TGC GAA GTT GAG CCT TGC AAA AAT GGT         576
Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys Lys Asn Gly
            180                 185                 190

GGA ATA TGT ACA GAT CTT GTT GCT AAC TAT TCC TGT GAG TGC CCA GGC         624
Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu Cys Pro Gly
        195                 200                 205

GAA TTT ATG GGA AGA AAT TGT CAA TAC AAA TGC TCA GGC CCA CTG GGA         672
Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly Pro Leu Gly
    210                 215                 220

ATT GAA GGT GGA ATT ATA TCA AAC CAG CAA ATC ACA GCT TCC TCT ACT         720
Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala Ser Ser Thr
225                 230                 235                 240

CAC CGA GCT CTT TTT GGA CTC CAA AAA TGG TAT CCC TAC TAT GCA CGT         768
His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr Tyr Ala Arg
                245                 250                 255

CTT AAT AAG AAG GGG CTT ATA AAT GCG TGG ACA GCT GCA GAA AAT GAC         816
Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala Glu Asn Asp
            260                 265                 270

AGA TGG AAG CGG TGG ATT CAG ATA AAT TTG CAA AGA AAA ATG AGA GTT         864
Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys Met Arg Val
        275                 280                 285

ACT GGT GTG ATT ACC CAA GGG GCC AAG AGG ATT GGA AGC CCA GAG TAT         912
Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro Glu Tyr
    290                 295                 300

ATA AAA TTC TAC AAA ATT GCC TAC AGT AAT GAT GGA AAG ACT TGG GCA         960
Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr Trp Ala
305                 310                 315                 320

ATG TAC AAA GTG AAA GGC ACC AAT GAA GAC ATG GTG TTT CGT GGA AAC        1008
Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg Gly Asn
                325                 330                 335

ATT GAT AAC AAC ACT CCA TAT GCT AAC TCT TTC ACA CCC CCC ATA AAA        1056
Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro Ile Lys
            340                 345                 350

GCT CAG TAT GTA AGA CTC TAT CCC CAA GTT TGT CGA AGA CAT TGC ACT        1104
Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His Cys Thr
        355                 360                 365

TTG CGA ATG GAA CTT CTT GGC TGT GAA CTG TCG GGT TGT TCT GAG CCT        1152
Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser Glu Pro
    370                 375                 380
```

```
CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG ATC ACT GCC TCC      1200
Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser
385                 390                 395                 400

AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA CCA AGG      1248
Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg
            405                 410                 415

AAA GCT CGG CTG GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC      1296
Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly
        420                 425                 430

CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC      1344
His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr
    435                 440                 445

AAA GTG ACT GGC ATC ATT ACA CAA GGA GCT AAA GAT TTT GGT CAT GTA      1392
Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val
450                 455                 460

CAG TTT GTT GGC TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC      1440
Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His
465                 470                 475                 480

TGG ACT GTA TAC CAG GAT GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG      1488
Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln
            485                 490                 495

GGA AAT TTT GAC AAT GAC ACT CAC AGA AAA AAT GTC ATC GAC CCT CCC      1536
Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro
        500                 505                 510

ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT TGG TCC TGG TAC GGG AGG      1584
Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg
    515                 520                 525

ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG GAG GAA TGA GGG      1632
Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu  *  Gly
    530                 535                 540

GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT ATC TCC      1680
Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser
545                 550                 555                 560

ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT      1728
Met Glu  *  Thr Val  *  Asn Leu  *  Glu Thr Glu Trp Phe Phe Phe
            565                 570                 575

TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT      1776
Phe Ser  *  Lys Ser Gly Gln Ile Met Val Gly Asn  *  Arg Cys Phe
            580                 585                 590

TAC C                                                                1780
Tyr
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys Arg
 1               5                  10              14
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Gly Lys Arg Thr Ser Ser
 1               5
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro
1               5                   10                  15

Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile
            20                  25                  30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
        35                  40                  45

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
    50                  55                  60

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
65                  70                  75                  80

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
                85                  90                  95

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
            100                 105                 110

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
        115                 120                 125

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
    130                 135                 140
```

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
145 150 155 160

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
165 170 175

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
180 185 190

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
195 200 205

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
210 215 220

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
225 230 235 240

Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
245 250 255

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
260 265 270

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
275 280 285

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
290 295 300

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
305 310 315 320

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
325 330 335

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
340 345 350

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
355 360 365

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
370 375 380

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
385 390 395 400

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu
405 410 415

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe
420 425 430

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
435 440 445

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
450 455 460

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
465 470 475 480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
500 505 510

Glu

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
1 5 10 15

Ser Met Glu

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTTATT 60

ACCCAAGGAG CAAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC 120

AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC 180

TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA 240

GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA 300

CTTCTTGGCT GTGAGCTC 318

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1 5 10 15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
35 40 45

His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
50 55 60

Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
65 70 75 80

Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu

85 90 95

Asp Gly Xaa Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp
100 105 110

Lys Glu Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met
115 120 125

Phe Asn Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser
130 135 140

Cys His Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu
145 150 155 160

His Gly Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp
165 170 175

Ser Gln Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala
180 185 190

Phe Gly Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Lys Ile
195 200 205

Asn Ala Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val
210 215 220

Asp Leu Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala
225 230 235 240

Arg Asp Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His
245 250 255

Ser Asp Asp Gly Val Gln Trp Thr Val Tyr Xaa Xaa Glu Glu Gln Gly
260 265 270

Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys
275 280 285

Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
290 295 300

Val Ser Trp His Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
1 5 10 15

Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp
20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
50 55 60

Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
65 70 75 80

Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
85 90 95

Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
100 105 110

Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
115 120 125

Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
130 135 140

Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
145 150 155 160

Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
165 170 175

Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
180 185 190

Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
195 200 205

Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
210 215 220

Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
225 230 235 240

Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
245 250 255

Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
260 265 270

Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
275 280 285

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
290 295 300

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
305 310 315 320

Thr

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1   5   10   15

Val Pro Gln Phe Gly Lys Gly Asp Ile
            20   25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1   5   10   15

Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
            20   25   30

Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
        35   40   45

Glu Glu Glu Pro Thr Ser Ala Gly Pro
    50   55

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1   5   10   15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
20 25 30

Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT     60

GTAGGTTCCT TTTCCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACTG TTCTAGTGTT    120

GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT    180

GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT    240

GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA    300

ATATGTACAG                                                           310
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 550...1212
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
GAATTCCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGGC CCAAAGCCAG CTAGGCTCAG     60

TCTCACACGC GCGCCGCCAC TGTTTGTATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC    120

CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC    180

GTGAGCCGTA GTCACTGCTG GCCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA    240

GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC    300

CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA    360

ATCACCCTTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCCAAGATTT GAGAAGCGCT    420

GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG    480

CGCGCCTCGC CTACTGTGCC CTCCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA    540

GAAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT GGA CTC AGC    591
          Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
           1               5                  10

CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC CCG AAC CCC      639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15                  20                  25                  30
```

```
TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT GAT TCC TTT      687
Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe
                35                  40                  45

TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC TCT AGT GTT      735
Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val
            50                  55                  60

GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA GGT CCC TGC      783
Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys
        65                  70                  75

ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA AGC GAA GCC      831
Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala
    80                  85                  90

TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT CCT CGG GGA      879
Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly
95                  100                 105                 110

TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT GAA GCT GAG      927
Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu
                115                 120                 125

CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT AAC TAC TCT      975
Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser
            130                 135                 140

TGT GAA TGC CCA GGA GAA TTT ATG GGA CGA AAT TGT CAA TAT AAA TGC     1023
Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys
        145                 150                 155

TCT GGG CAC TTG GGA ATC GAA GGT GGG ATC ATA TCT AAT CAG CAA ATC     1071
Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile
    160                 165                 170

ACA GCT TCA TCT AAT CAC CGA GCT CTT TTT GGA CTC CAG AAG TGG TAT     1119
Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr
175                 180                 185                 190

CCC TAC TAT GCT AGA CTT AAT AAG AAG GGC CTT ATA AAT GCC TGG ACA     1167
Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr
                195                 200                 205

GCT GCT GAA AAT GAC AGA TGG CCA TGG ATT CAG GTA ACA GTG GGA TGAGA  1217
Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
            210                 215                 220

CAAATCCATT TCCCAAATTA TCAGAATCAT TATAGAAGTA GGTTAGGGAG AATTGGCTGT   1277

GATTCTTTCT CATGGTTAAA ATGTGATTTA GTTCAGAATT AACATGGTTG GAAACTCTAA   1337

AAAATGTGGA AAACAGGAAC ATTCTATGTC TGAAAATCTG AAAATAGCAT CAAGATGAAA   1397

ACATTCTTTA GTCATAAATA TACTCTTTTA AGTTATAGTA GAGAAAAAGA TCTTATCATT   1457

TCATAAGTGG ACTTTTGGGA TAGCATTGGA AATGTAAATG AAATAAATAC CTAATTGAAA   1517

AAAGTTTATT CTAAAGTGTT AATATTTAGC AACAGATTCA GAGACAAGAA AGTAACAATT   1577

CAATCTGTGT ATTTTTTGTG AGAAATAGTT TCCCATGTGC AAATATAAAG TGCGCATCAT   1637

ATCATGATAA TATCCAACTG TCTGCAGAAC TCCCTTTCAT AAATGAGAGA ATTTTAATTC   1697
```

ATAGTGCCTT ATATCCTCAT CAGCCATCTG ACTTTACTAC AGAAGAAAAC AATGAAATGA 1757

TGCATTAAGT GCTTTGCTAG AAGAAACATC ATAGCAAAGC TGATAGCCCA CATTCTGTGC 1817

ANNNAAGCTT CCAGAGCACT CGAGAAAAAG CAGAAATGAG ATGTTTTATG AAAACCGAAA 1877

AGATAATCTG ATTTCTGTGA AATATACTTT TGATCATGTG GTTCTTTAAG ATAGTCACTA 1937

ACAAGTCATT AGTAGCAGAT ACCAAATGGG AGAAAATTTC CAGTATACTG AGGGTCAAGG 1997

CAGTCATGCT GAAACTACAT GAGGTCAGGA AAGTTTTGAA ATAAGGTGAT TTTGGAAGGA 2057

TACCTTCAAC TGGCCTAGAT TTTCAAGAAA CAGTGTAATC AACAGCCAAA CATGAGAATC 2117

TAGCTAACAG CATTTAGAAA ACCAGAACTA AGAGTGTTAC TGGGGAATTG CATTTAAATC 2177

CAGTATGAGA GTTTGCAAAT GCCGTATTCT TCTAAGGGGT TTGTGCCACA TTTTGTTACC 2237

ATGGAGTCCT CTGTAAGAAC TTTATTAGAT AAATCATCTT TACACTATAA TTTGAATAAA 2297

AGCCGGAATT C 2308

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115 120 125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly

145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

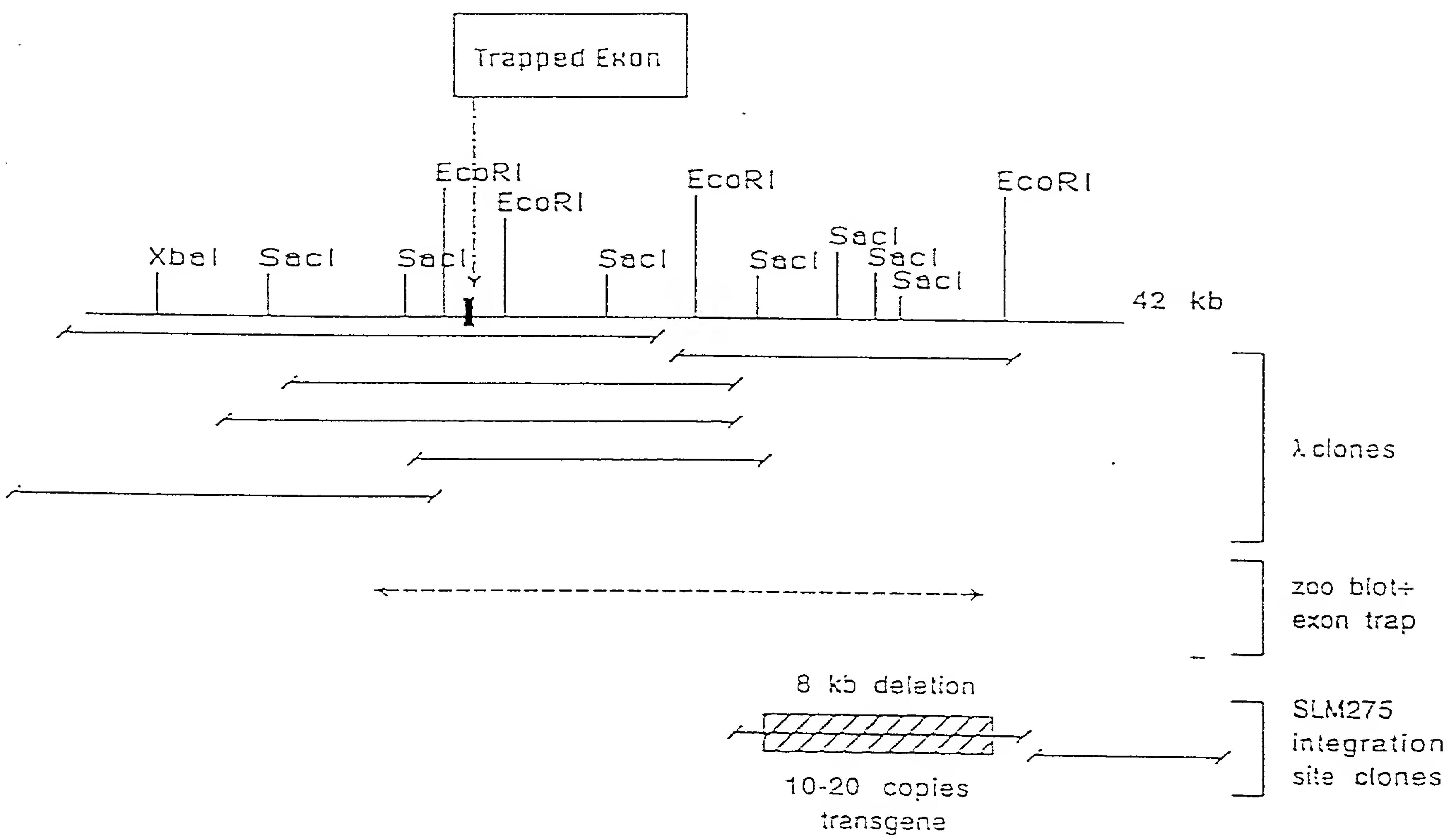
Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Ala Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
210 215 220

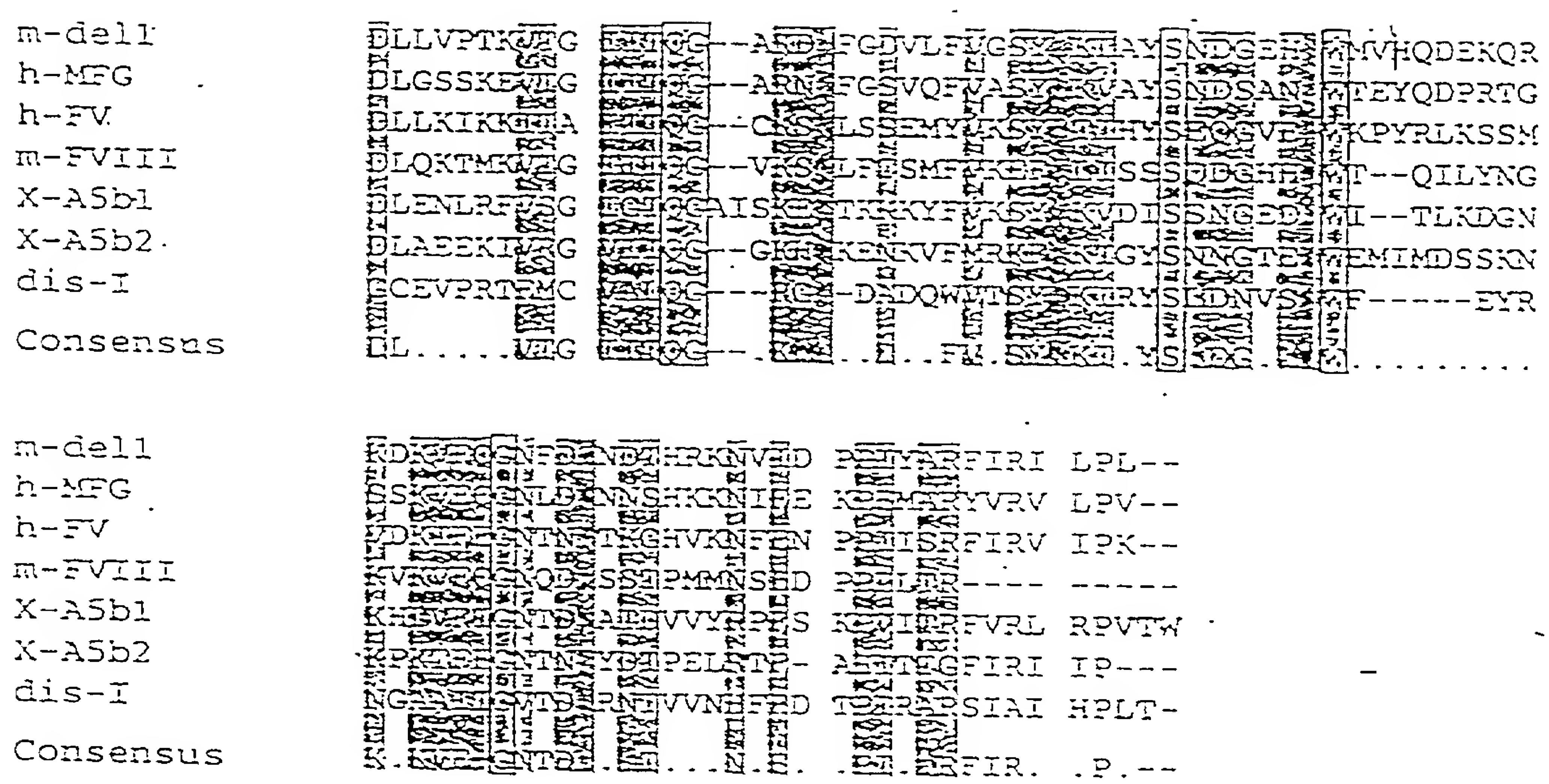
8907-034 (Sheet 1 of 32)

Figure 1



8907-034 (sheet 2 of 32)

Figure 2



8907-034 (sheet 3 of 32)

Figure 3A

```
         10          20          30          40          50          60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

EcoRI       HpaI
GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA      60

                      DraI
TTCCCAGTGG CCTTGATATT TAAACTGATT CCTGCCACCA GGTCCTTGGG CCACCCTGTC     120

           Esp3I       SphI
CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCGCTCC TGGCCTCAGG     180

CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCG     240

                                                 BssHII
CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGCGTGCGCG CACGGAAATC     300

GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC     360

AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG     420

TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTG     480
```

8907-034 (Sheet - of 32)

Figure 33

```
         10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

     Eco47III                  AatII
AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG     540

        BssHII
      PstI
TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCCGGACCA GCCCAGGTCA     600

                   BspHI
CGTCCGTGAG AAGGGATCAT GAAGCACTTG GTAGCAGCCT GGCTTTTGGT TGGACTCAGC     660
                      M  K  H  L   V  A  A  W   L  L  V   G  L  S

CTCGGGGTGC CCCAGTTCGG CAAAGGTGAC ATTTGCAACC CGAACCCCTG TGAAAATGGT     720
L  G  V  P   Q  F  G   K  G  D   I  C  N  P   N  P  C   E  N  G

                                                       BspMI
GGCATCTGTC TGTCAGGACT GGCTGATGAT TCCTTTTCCT GTGAGTGTCC AGAAGGCTTC     780
G  I  C  L   S  G  L   A  D  D   S  F  S  C   E  C  P   E  G  F

                                                       BspMI
GCAGGTCCGA ACTGCTCTAG TGTTGTGGAG GTTGCATCAG ATGAAGAAAA GCCTACTTCA     840
A  G  P  N   C  S  S   V  V  E   V  A  S  D   E  E  K   P  T  S

GCAGGTCCCT GCATCCCTAA CCCATGCCAT AACGGAGGAA CCTGTGAGAT AAGCGAAGCC     900
A  G  P  C   I  P  N   P  C  H   N  G  G  T   C  E  I   S  E  A

TATCGAGGAG ACACATTCAT AGGCTATGTT TGTAAATGTC CTCGGGGATT TAATGGGATT     960
Y  R  G  D   T  F  I   G  Y  V   C  K  C  P   R  G  F   N  G  I
```

Figure 3C

```
          10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

CACTGTCAGC ACAATATAAA TGAATGTGAA GCTGAGCCTT GCAGAAATGG CGGAATATGT   1020
H  C  Q  H   N  I  N   E  C  E   A  E  P  C   R  N  G   G  I  C

                                    BsmI
ACCGACCTTG TTGCTAACTA CTCTTGTGAA TGCCCAGGAG AATTTATGGG ACGAAATTGT   1080
T  D  L  V   A  N  Y   S  C  E   C  P  G  E   F  M  G   R  N  C

CAATATAAAT GCTCTGGGCA CTTGGGAATC GAAGGTGGGA TCATATCTAA TCAGCAAATC   1140
Q  Y  K  C   S  G  H   L  G  I   E  G  G  I   I  S  N   Q  Q  I

                         SacI
                       Ecl136II
ACAGCTTCAT CTAATCACCG AGCTCTTTTT GGACTCCAGA AGTGGTATCC CTACTATGCT   1200
T  A  S  S   N  H  R   A  L  F   G  L  Q  K   W  Y  P   Y  Y  A

                                                              NcoI
                                                              MscI
                                          PvuII               BalI
CGACTTAATA AGAAGGGCCT TATAAATGCC TGGACAGCTG CTGAAAATGA CAGATGGCCA   1260
R  L  N  K   K  G  L   I  N  A   W  T  A  A   E  N  D   R  W  P

TGGATTCAGA TAAATTTGCA AAGAAAAATG AGAGTCACTG GTGTTATTAC CCAAGGAGCA   1320
W  I  Q  I   N  L  Q   R  K  M   R  V  T  G   V  I  T   Q  G  A

AAAAGGATTG GAAGCCCAGA GTACATAAAA TCCTACAAAA TTGCCTACAG CAATGACGGG   1380
K  R  I  G   S  P  E   Y  I  K   S  Y  K  I   A  Y  S   N  D  G

      BbsI                          EarI
AAGACCTGGG CAATGTACAA AGTAAAAGGC ACCAATGAAG AGATGGTCTT TCGTGGAAAT   1440
K  T  W  A   M  Y  K   V  K  G   T  N  E  E   M  V  F   R  G  N
```

8907-034 (sheet 6 of 32)

Figure 3D

```
         10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

                  NdeI
GTTGATAACA ACACACCATA TGCTAATTCT TTCACACCCC CAATCAAAGC TCAGTATGTA   1500
V  D  N  N   T  P  Y   A  N  S   F  T  P  P   I  K  A   Q  Y  V

AGACTCTACC CCCAAATTTG TCGAAGGCAT TGTACTTTAA GAATGGAACT TCTTGGCTGT   1560
R  L  Y  P   Q  I  C   R  R  H   C  T  L  R   M  E  L   L  G  C

   SacI
  Ecl136II
GAGCTCTCAG GCTGTTCAGA ACCTTTGGGG ATGAAATCAG GGCATATACA AGACTACCAG   1620
E  L  S  G   C  S  E   P  L  G   M  K  S  G   H  I  Q   D  Y  Q

         BbsI
ATCACTGCCT CCAGCGTCTT CAGAACACTC AACATGGACA TGTTTACTTG GGAACCAAGG   1680
I  T  A  S   S  V  F   R  T  L   N  M  D  M   F  T  W   E  P  R

AAAGCCAGGC TGGACAAGCA AGGCAAAGTA AATGCCTGGA CTTCCGGCCA TAACGACCAG   1740
K  A  R  L   D  K  Q   G  K  V   N  A  W  T   S  G  H   N  D  Q

TCACAATGGT TACAGGTTGA TCTTCTTGTC CCTACTAAGG TGACAGGCAT CATTACACAA   1800
S  Q  W  L   Q  V  D   L  L  V   P  T  K  V   T  G  I   I  T  Q

                       PmlI
GGAGCTAAAG ATTTTGGTCA CGTGCAGTTT GTTGGGTCAT ACAAACTAGC TTACAGCAAT   1860
G  A  K  D   F  G  H   V  Q  F   V  G  S  Y   K  L  A   Y  S  N

                   ApaLI
GATGGAGAAC ACTGGATGGT GCACCAGGAT GAAAAACAGA GGAAAGACAA GGTTTTTCAA   1920
D  G  E  H   W  M  V   H  Q  D   E  K  Q  R   K  D  K   V  F  Q
```

8907-034 (Sheet 7 of 32)

Figure 3E

```
         10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

GGCAATTTTG ACAATGACAC TCACAGGAAA AATGTCATCG ACCCTCCCAT CTATGCACGA   1980
G  N  F  D   N  D  T   H  R  K   N  V  I  D   P  P  I   Y  A  R

TTCATAAGAA TCCTTCCTTG GTCCTGGTAT GGAAGGATCA CTCTGCGGTC AGAGCTGCTG   2040
F  I  R  I   L  P  W   S  W  Y   G  R  I  T   L  R  S   E  L  L

   FspI
GGCTGCGCAG AGGAGGAATG AAGTGCGGGG CCGCACATCC CACAATGCTT TTCTTTATTT   2100
G  C  A  E   E  E

TCCTATAAGT ATCTCCACGA AATGAACTGT GTGAAGCTGA TGGAAACTGC ATTTGTTTTT   2160

                                                       HindIII
TTCAAAGTGT TCAAATTATG GTAGGCTACT GACTGTCTTT TTAGGAGTTC TAAGCTTGCC   2220

TTTTTAATAA TTTAATTTGG TTTCCTTTGC TCAACTCTCT TATGTAATAT CACACTGTCT   2280

                EarI
GTGAGTTACT CTTCTTGTTC TCT                                           2303
```

8907-034 (Sheet 8 of 32)

Figure 4A

```
            9           18          27          36          45          54
5' TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG CGC TGA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    S   L   *   S   P   L   S   P   S   P   R   I   C   L   T   K   R   *

            63          72          81          90          99          108
   GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT CTG CTG CTG CCC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   K   R   T   S   S   *   I   L   *   *   G   R   S   L   L   L   P

            117         126         135         144         153         162
   TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG ACC CCT GAC CAG CCG GGG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    C   A   A   T   S   A   T   L   P   S   A   T   T   P   D   Q   P   G

            171         180         189         198         207         216
   TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC TCG GTA GCC GTC TGG CTC TTG GTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    S   R   P   G   D   G   I   M   K   R   S   V   A   V   W   L   L   V

            225         234         243         252         261         270
   GGG CTC AGC CTC GGT GTC CCC CAG TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   L   S   L   G   V   P   Q   F   G   K   G   D   I   C   D   P   N

            279         288         297         306         315         324
   CCA TGT GAA AAT GGA GGT ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    P   C   E   N   G   G   I   C   L   P   G   L   A   V   G   S   F   S

            333         342         351         360         369         378
   TGT GAG TGT CCA GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    C   E   C   P   D   G   F   T   D   P   N   C   S   S   V   V   E   V

            387         396         405         414         423         432
   GCA TCA GAT GAA GAA GAA CCA ACT TCA GCA GGT CCC TGC ACT CCT AAT CCA TGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A   S   D   E   E   E   P   T   S   A   G   P   C   T   P   N   P   C

            441         450         459         468         477         486
   CAT AAT GGA GGA ACC TGT GAA ATA AGT GAA GCA TAC CGA GGG GAT ACA TTC ATA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    H   N   G   G   T   C   E   I   S   E   A   Y   R   G   D   T   F   I

            495         504         513         522         531         540
   GGC TAT GTT TGT AAA TGT CCC CGA GGA TTT AAT GGG ATT CAC TGT CAG CAC AAC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   Y   V   C   K   C   P   R   G   F   N   G   I   H   C   Q   H   N

            549         558         567         576         585         594
   ATA AAT GAA TGC GAA GTT GAG CCT TGC AAA AAT GGT GGA ATA TGT ACA GAT CTT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    I   N   E   C   E   V   E   P   C   K   N   G   G   I   C   T   D   L

            603         612         621         630         639         648
   GTT GCT AAC TAT TCC TGT GAG TGC CCA GGC GAA TTT ATG GGA AGA AAT TGT CAA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   A   N   Y   S   C   E   C   P   G   E   F   M   G   R   N   C   Q
```

```
                657         666         675         684         693         702
TAC AAA TGC TCA GGC CCA CTG GGA ATT GAA GGT GGA ATT ATA TCA AAC CAG CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   K   C   S   G   P   L   G   I   E   G   G   I   I   S   N   Q   Q

                711         720         729         738         747         756
ATC ACA GCT TCC TCT ACT CAC CGA GCT CTT TTT GGA CTC CAA AAA TGG TAT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   T   A   S   S   T   H   R   A   L   F   G   L   Q   K   W   Y   P

                765         774         783         792         801         810
TAC TAT GCA CGT CTT AAT AAG AAG GGG CTT ATA AAT GCG TGG ACA GCT GCA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   Y   A   R   L   N   K   K   G   L   I   N   A   W   T   A   A   E

                819         828         837         846         855         864
AAT GAC AGA TGG AAC CGG TGG ATT CAG ATA AAT TTG CAA AGA AAA ATG AGA GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   D   R   W   N   R   W   I   Q   I   N   L   Q   R   K   M   R   V

                873         882         891         900         909         918
ACT GGT GTG ATT ACC CAA GGG GCC AAG AGG ATT GGA AGC CCA GAG TAT ATA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   G   V   I   T   Q   G   A   K   R   I   G   S   P   E   Y   I   K

                927         936         945         954         963         972
TTC TAC AAA ATT GCC TAC AGT AAT GAT GGA AAG ACT TGG GCA ATG TAC AAA GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   Y   K   I   A   Y   S   N   D   G   K   T   W   A   M   Y   K   V

                981         990         999        1008        1017        1026
AAA GGC ACC AAT GAA GAC ATG GTG TTT CGT GGA AAC ATT GAT AAC AAC ACT CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   G   T   N   E   D   M   V   F   R   G   N   I   D   N   N   T   P

               1035        1044        1053        1062        1071        1080
TAT GCT AAC TCT TTC ACA CCC CCC ATA AAA GCT CAG TAT GTA AGA CTC TAT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   A   N   S   F   T   P   P   I   K   A   Q   Y   V   R   L   Y   P

               1089        1098        1107        1116        1125        1134
CAA GTT TGT CGA AGA CAT TGC ACT TTG CGA ATG GAA CTT CTT GGC TGT GAA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   V   C   R   R   H   C   T   L   R   M   E   L   L   G   C   E   L

               1143        1152        1161        1170        1179        1188
TCG GGT TGT TCT GAG CCT CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   C   S   E   P   L   G   M   K   S   G   H   I   Q   D   Y   Q

               1197        1206        1215        1224        1233        1242
ATC ACT GCC TCC AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   T   A   S   S   I   F   R   T   L   N   M   D   M   F   T   W   E

               1251        1260        1269        1278        1287        1296
CCA AGG AAA GCT CGG CTC GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   R   K   A   R   L   D   K   Q   G   K   V   N   A   W   T   S   G

               1305        1314        1323        1332        1341        1350
CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC AAA GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   N   D   Q   S   Q   W   L   Q   V   D   L   L   V   P   T   K   V
```

8907-034 (Sheet 10 of 32)

Figure 4c

```
        1359         1368         1377         1386         1395         1404
ACT GGC ATC ATT ACA CAA GCA GCT AAA GAT TTT GGT CAT GTA CAG TTT GTT GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   G   I   I   T   Q   G   A   K   D   F   G   H   V   Q   F   V   G

        1413         1422         1431         1440         1449         1458
TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC TGG ACT GTA TAC CAG GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Y   K   L   A   Y   S   N   D   G   E   H   W   T   V   Y   Q   D

        1467         1476         1485         1494         1503         1512
GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG GGA AAT TTT GAC AAT GAC ACT CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   K   Q   R   K   D   K   V   F   Q   G   N   F   D   N   D   T   H

        1521         1530         1539         1548         1557         1566
AGA AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   K   N   V   I   D   P   P   I   Y   A   R   H   I   R   I   L   P

        1575         1584         1593         1602         1611         1620
TGG TCC TGG TAC GGG AGG ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   S   W   Y   G   R   I   T   L   A   S   E   L   L   G   C   T   E

        1629         1638         1647         1656         1665         1674
GAG GAA TGA GGG GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   *   G   E   A   T   F   H   N   R   L   P   Y   L   G   K   S

        1683         1692         1701         1710         1719         1728
ATC TCC ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   S   M   E   *   T   V   *   N   L   *   E   T   E   W   F   F   F

        1737         1746         1755         1764         1773
TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT TAC C 3'
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -
 F   S   *   K   S   G   Q   I   M   V   G   N   *   R   C   F   Y
```

Figure 5

```
        10         20         30         40         50         60
GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTTATT

        70         80         90        100        110        120
ACCCAAGGAG CAAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC

       130        140        150        160        170        180
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC

       190        200        210        220        230        240
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA

       250        260        270        280        290        300
GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA

       310        320        330        340        350        360
CTTCTTGGCT GTGAGCTC.. .......... .......... .......... ..........
```

8907-034 (Sheet 12 of 32)

Figure 6

```
                                               egf-1
m-del-1  MKHLVAAWLLVGLSLGVPQFGKGDICNPNPCENGGICLSGLADDSFSCEC    50
h-del-1    RS   V                  D           P   VG
                                          egf-2
m-del-1  PEGFAGPNCSSVVEVASDEEKPTSAGPCIPNPCHNGGTCEISEAYRGDTF   100
h-del-1   D   TD              E       T
                                               egf-3
m-del-1  IGYVCKCPRGFNGIHCQHNINECEAEPCKNGGICTDLVANYSCECPGEFM   150
h-del-1                          V   K

m-del-1  GRNCQYKCSGHLGIEGGIISNQQITASSNHRALFGLQKWYPYYARLNKKG   200
h-del-1             P                T
                                               discoidin-1
m-del-1  LINAWTAAENDRWP-WIQENLQRKMRVTGVITQGAKRIGSPEYIKSYKIA   249
h-del-1               NR    +VTVG = 'minor'           F       250

m-del-1  YSNDGKTWAMYKVKGTNEEMVFRGNVDNNTPYANSFTPPIKAQYVRLYPQ   299
h-del-1                    D      I                           300

m-del-1  ICRRHCTLRMELLGCELSGCSEPLGMKSGHIQDYQITASSVFRTLNMDMF   349
h-del-1  V                                       I            350
                         discoidin-2
m-del-1  TWEPRKARLDKQGKVNAWTSGHNDQSQWLQVDLLVPTKVTGIITQGAKDF   399
h-del-1                                 K                 K   400

m-del-1  GHVQFVGSYKLAYSNDGEHWMVHQDEKQRKDKVFQGNFDNDTHRKNVIDP   449
h-del-1                      T K          K                   450

m-del-1  PIYARFIRILPWSWYGRITLRSELLGCAEEE   430
h-del-1        H             A      T      481
```

8907-034 (Sheet 13 of 32)

Figure 7

PROTEIN DOMAINS OF HUMAN DEL-1

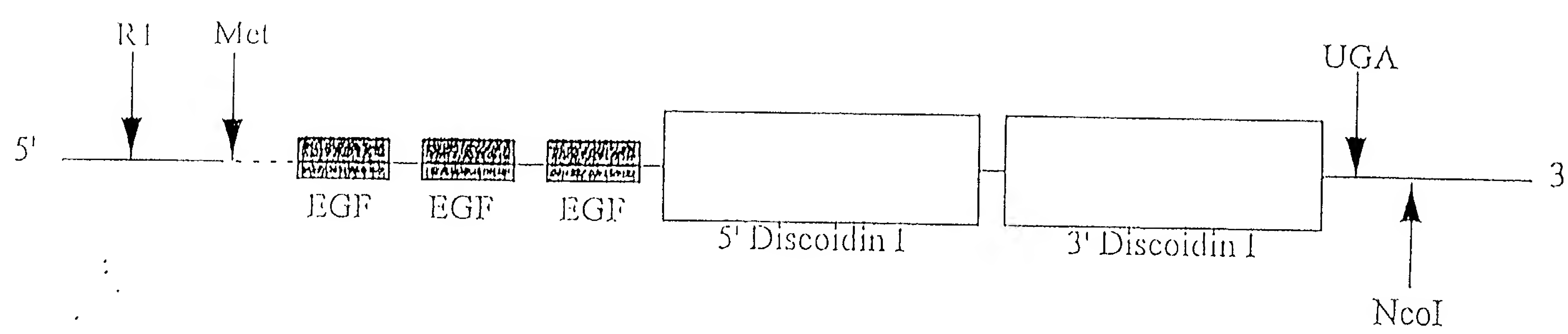


Figure 8

```
      1        10        20        30        40        50        60        70
   N- CSTQLGMEGGAIADSQISASYVYMGFMGLQRWGPELARLYRTGIVNAWHASNYD-SKPWIQVNLLRRMRV
      **  ** *** *    ** **          *** * *  ***    *  *** *   *      *** ** *****
   N- CSGPLGIEGGIISNQQITASSTHRALFGLQKWYPYYARLNKKGLINAWTAAENDRWNRWIQINLQRKMRV
      1        10        20        30        40        50        60        70

     71       80        90       100       110       120       130       140
      SGVMTQGASRAGRAEYLNTFKVAYSLDG-RKFEFIQDESGGDKEFLGNLDNNSLKVNMFNPTLEAQYIRL
       ** **** * *  ** *  * *** **                 *  * ** ***    * * *   *** **
      TGVITQGAKRIGSPEYIKFYKIAYSNDGKTWAMYKVKGTNEDMVFRGNIDNNTPYANSFTPPIKAQYVRL
     71       80        90       100       110       120       130       140

    141      150       160       170       180       190       200       210
      YFVSCHRGCTLRFELLGCELHGCLEPLGLKNNTIPDSQMSASSSYKTWNLRAFGWYPHLGRLDNQGKING
      **   * * **** ******* ** **** *   * * *  ***   * *   * * *    *** *** **
      YPQVCRRHCTLRMELLGCELSGCSEPLGMKSGHIQDYQITASSIFRTLNMDMFTWEPRKARLDKQGKVNA
    141      150       160       170       180       190       200       210

    211      220       230       240       250       260       270       280
      WTAQSNSAKEWLQVDLGTQRQVTGIITQGARDFGHIQYVESYKVAHSDDGVQWTVY--EEQGSSKVFQGN
      **   *    ******     ********* **** * * *** * * **  ****  * *   ******
      WTSGHNDQSQWLQVDLLVPTKVTGIITQGAKDFGHVQFVGSYKLAYSNDGEHWTVYQDEKQRKDKVFQGN
    211      220       230       240       250       260       270       280

    281      290       300       310       320
      LDNNSHKKNIFEKPFMARYVRVLPVSWHNRITLRLELLGC*  -C
       **  * **     *  **  * ** **  ****  *****
      FDNDTHRRNVIDPPIYARHIRILPWSWYGRITLRSELLGCT  -C
    281      290       300       310       320
```

8907-034 (Sheet 15 of 32)

Figure 9

PUTATIVE SIGNAL SEQUENCE OF HUMAN DEL-1

M K R S V A V W L L V G L S L G V P Q F G K G D I ...

8907-034 (Sheet 16 of 32)

Figure 10

EGF-like Domains of hu Del-1

```
     1)        CDPNPCENGGICLPGLAVG-----SFSCECPDGFTDPNCS  SVVEVASDEEEPTSAGP
     2)        CTPNPCHNGGTCEISEAYRGDTFIGYVCKCPRGFNGIHCQ  HNINE
     3)        CEVEPCKNGGICTDLVA-------NYSCECPGEFMGRNCQ  YK

CONSENSUS      C---PC-NGG-C-------------Y-C-C--GY-G--C-
EGF DOMAIN                              F        F
```

Figure 11

```
                9                18                27                36                45                54
5' -GT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT ATC TGT TTG CCA GGA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    X   D   I   C   D   P   N   P   C   E   N   G   G   I   C   L   P   G

               63                72                81                90                99               108
   TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA GAT GGC TTC ACA GAC CCC AAC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   A   V   G   S   F   S   C   E   C   P   D   G   F   T   D   P   N

              117               126               135               144               153               162
   TGT TCT AGT GTT GTG GAG GTT GGT CCC TGC ACT CCT AAT CCA TGC CAT AAT GGA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    C   S   S   V   V   E   V   G   P   C   T   P   N   P   C   H   N   G

              171               180               189               198               207               216
   GGA ACC TGT GAA ATA AGT GAA GCA TAC CGA GGG GAT ACA TTC ATA GGC TAT GTT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   T   C   E   I   S   E   A   Y   R   G   D   T   F   I   G   Y   V

              225               234               243               252               261               270
   TGT AAA TGT CCC CGA GGA TTT AAT GGG ATT CAC TGT CAG CAC AAC ATA AAT GAA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    C   K   C   P   R   G   F   N   G   I   H   C   Q   H   N   I   N   E

              279               288               297               306
   TGC GAA GTT GAG CCT TGC AAA AAT GGT GGA ATA TGT ACA G 3'
   --- --- --- --- --- --- --- --- --- --- --- --- --- -
    C   E   V   E   P   C   K   N   G   G   I   C   T
```

Figure 12A

```
         10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

 EcoRI                                    SacII    ApaI
GAATTCCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGGC CCAAAGCCAG CTAGGCTCAG      60

TCTCACACGC GCGCCGCCAC TGTTTGTATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC     120

CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC     180

GTGAGCCGTA GTCACTGCTG GCCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA     240

GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC     300

CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA     360

                                                       Eco47III
ATCACCCTTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCCAAGATTT GAGAAGCGCT     420

              AatII                                         PstI
GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG     480
```

8907-034 (Sheet 19 of 32)
Figure 12B

```
        10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890


CGCGCCTCGC CTACTGTGCC CTCCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA     540


            BspHI
GAAGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGACTCAG CCTCGGGGTG     600
           M  K  H  L   V  A  A  W  L  L  V   G  L  S   L  G  V


CCCCAGTTCG GCAAAGGTGA CATTTGCAAC CCGAACCCCT GTGAAAATGG TGGCATCTGT     660
P  Q  F  G   K  G  D   I  C  N   P  N  P  C   E  N  G   G  I  C


                                             BspMI
CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGTC CAGAAGGCTT CGCAGGTCCG     720
L  S  G  L   A  D  D   S  F  S   C  E  C  P   E  G  F   A  G  P


                                             BspMI
AACTGCTCTA GTGTTGTGGA GGTTGCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC     780
N  C  S  S   V  V  E   V  A  S   D  E  E  K   P  T  S   A  G  P


TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA     840
C  I  P  N   P  C  H   N  G  G   T  C  E  I   S  E  A   Y  R  G


GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG     900
D  T  F  I   G  Y  V   C  K  C   P  R  G  F   N  G  I   H  C  Q


CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT     960
H  N  I  N   E  C  E   A  E  P   C  R  N  G   G  I  C   T  D  L
```

8907-034 (Sheet 20 of 32)
Figure 12C

```
         10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890


                           BsmI
GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA    1020
V  A  N  Y   S  C  E   C  P  G   E  F  M  G   R  N  C   Q  Y  K


TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA    1080
C  S  G  H   L  G  I   E  G  G   I  I  S  N   Q  Q  I   T  A  S

                SacI
               Ecl136II
TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT    1140
S  N  H  P   A  L  F   G  L  Q   K  W  Y  P   Y  Y  A   R  L  N
                                                 NcoI
                                                 MscI
                             PvuII               BalI
AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTCAG    1200
N  K  G  L   I  N  A   W  T  A   A  E  N  D   R  W  P   W  I  Q


GTAACAGTGG GATGAGACAA ATCCATTTCC CAAATTATCA GAATCATTAT AGAAGTAGGT    1260
V  T  V  G   .


TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTTAAAATG TGATTTAGTT CAGAATTAAC    1320


ATGGTTGGAA ACTCTAAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA    1380


ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG    1440
```

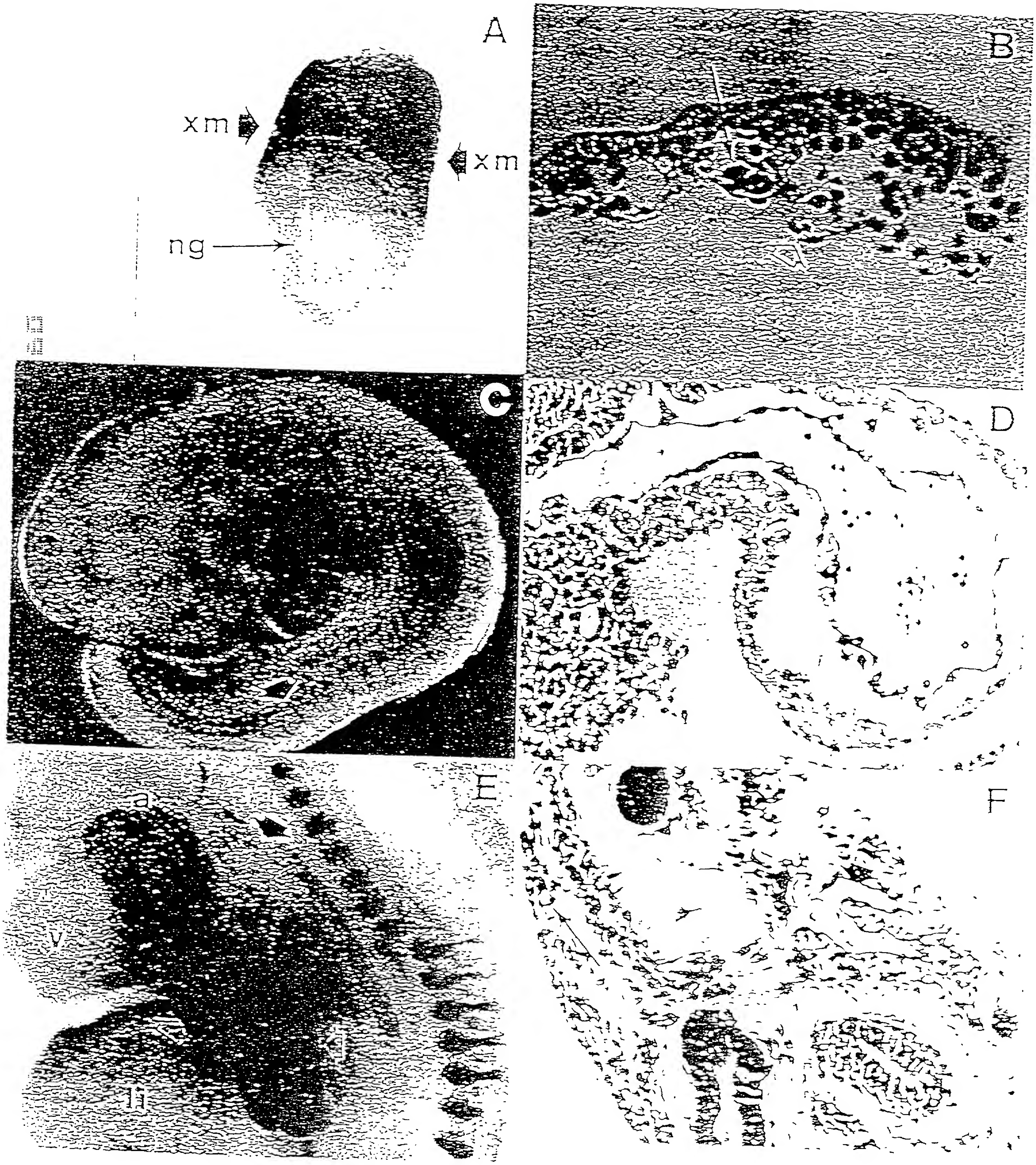
8907-034 (Sheet 21 of 32)
Figure 12D

```
        10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

    BglII
AAAAAGATCT TATCATTTCA TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA    1500

                                            SspI
TAAATACCTA ATTGAAAAAA GTTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTCAGAG    1560

ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTTGTGAGA AATAGTTTCC CATGTGCAAA    1620

          FspI      BspHI                       PstI
TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA    1680

TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTACTACAGA    1740

                      NsiI
AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA   -1800

                                  XhoI
                      HindIII     PaeR7I
TAGCCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAAGCAG AAATGAGATG    1860

                                                  BclI
TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT    1920
```

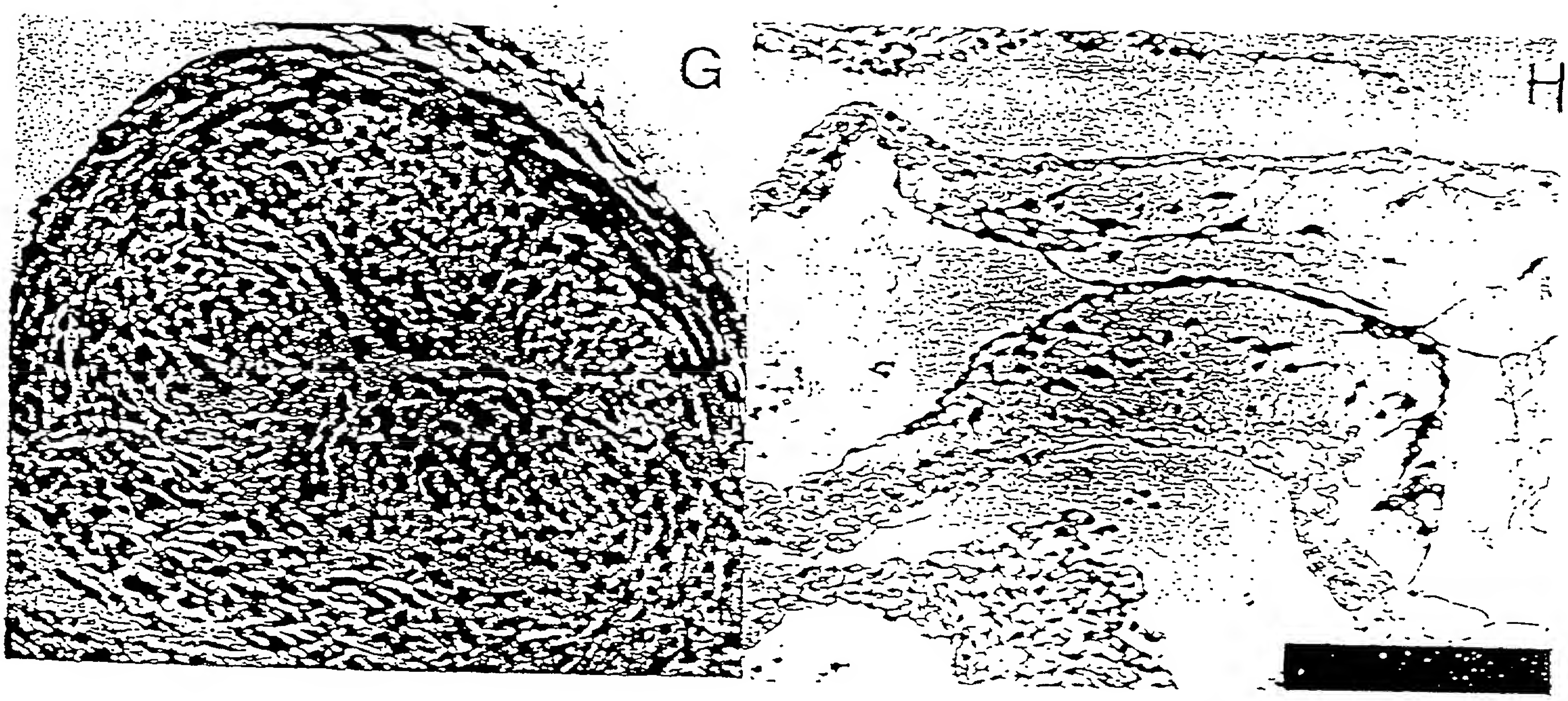
Figure 12E

```
         10         20         30         40         50         60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890


CTTTAAGATA GTCACTAACA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG    1980

   Bst1107I
TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAAG TTTTGAAATA    2040

AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAATCAAC    2100

AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG    2160

                DraI
GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG    2220

                     NcoI
TGCCACATTT TGTTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC    2280

                                 EcoRI
ACTATAATTT GAATAAAAGC CGGAATTC                                       2308
```

8907-034 (Sheet 23 of 32)
Figure 3A - 3F

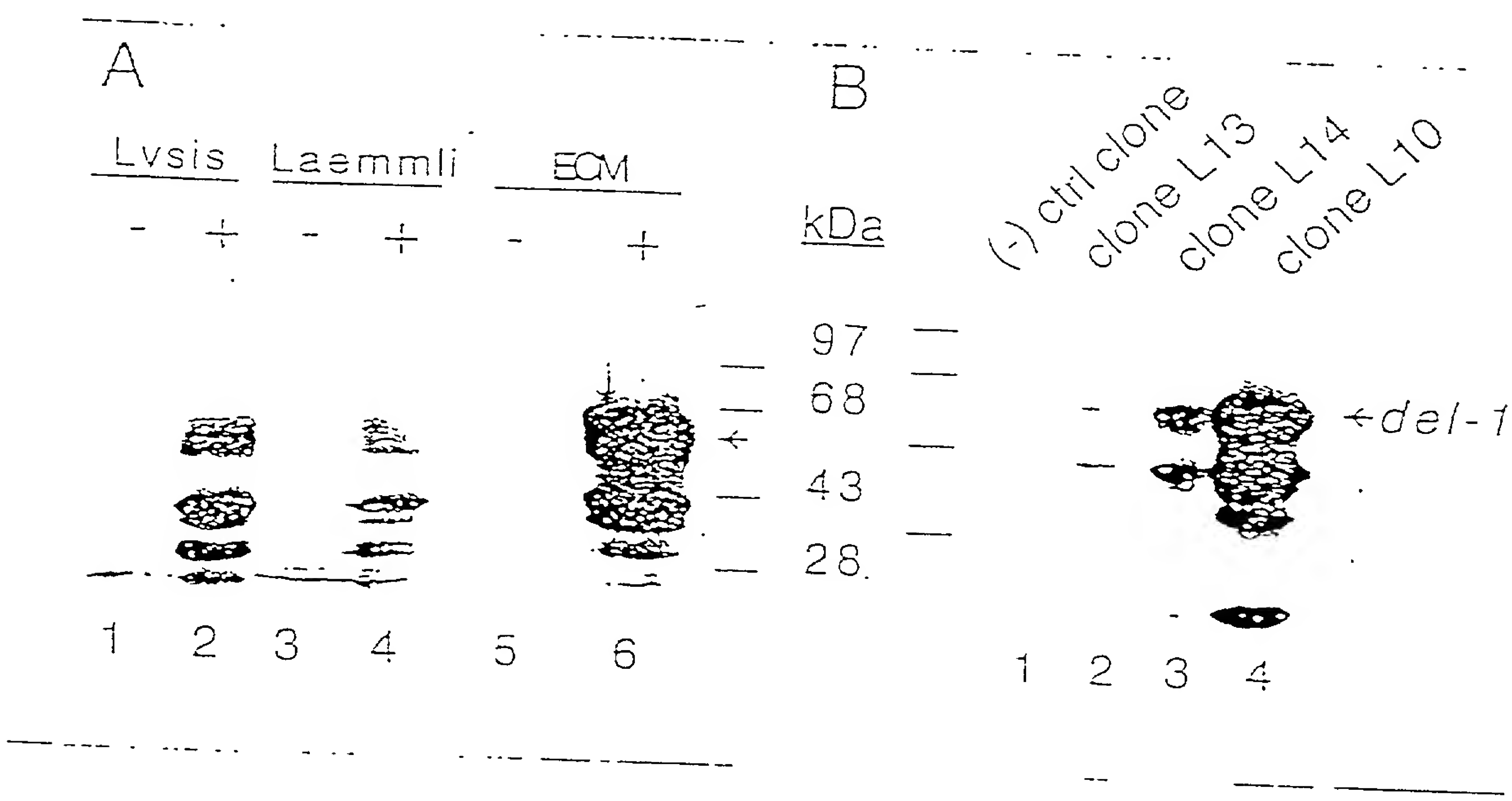


8907-034 (Sheet 24 of 32)
Figure 13G and 13H



8907-034 (Sheet 25 of 32)

Figure 14A and 14B



8907-034 (Sheet 26 of 32)

Figure 15A

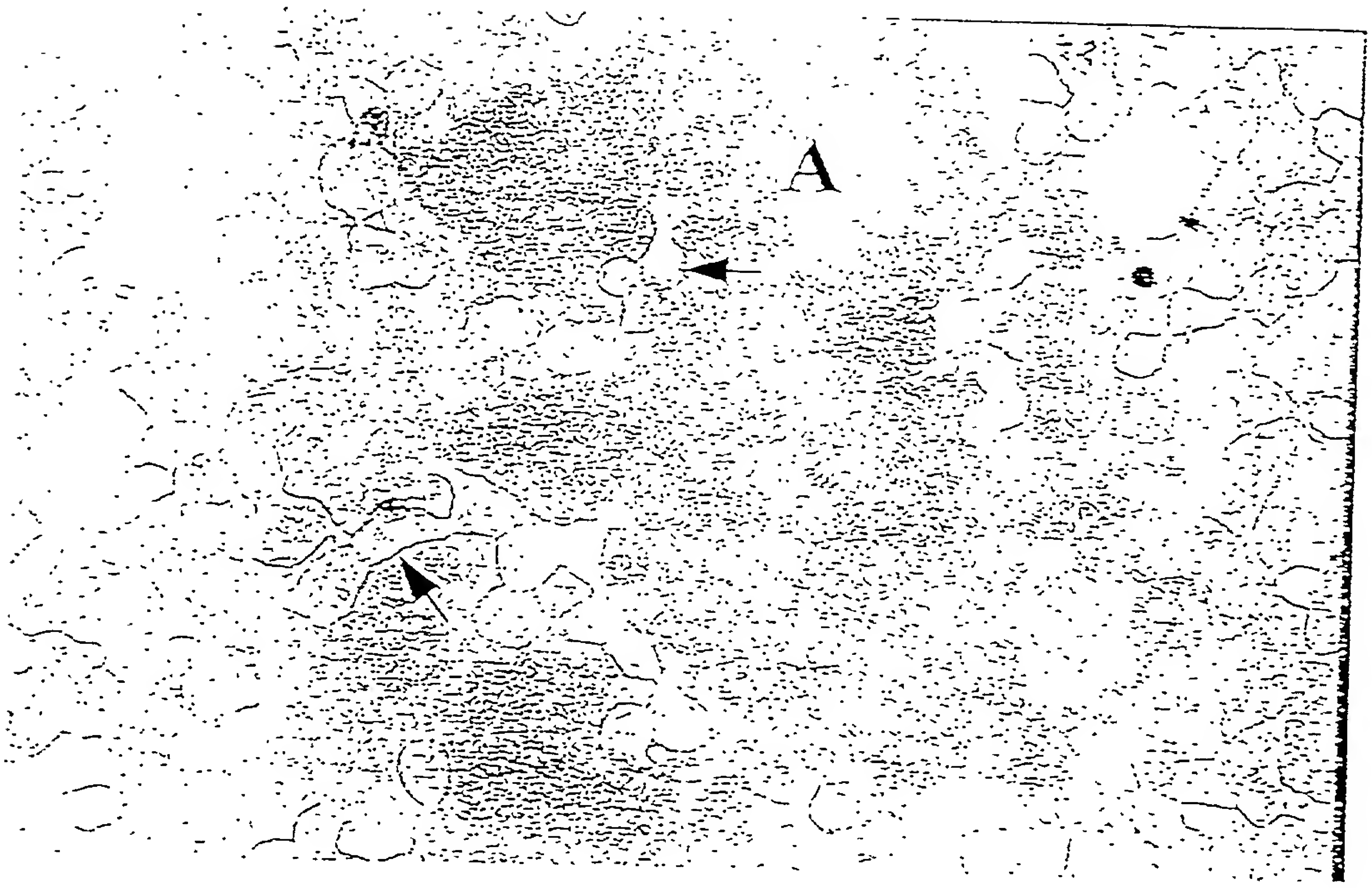


Figure 15B

8907-034 (Sheet 27 of 32)

Figure 16

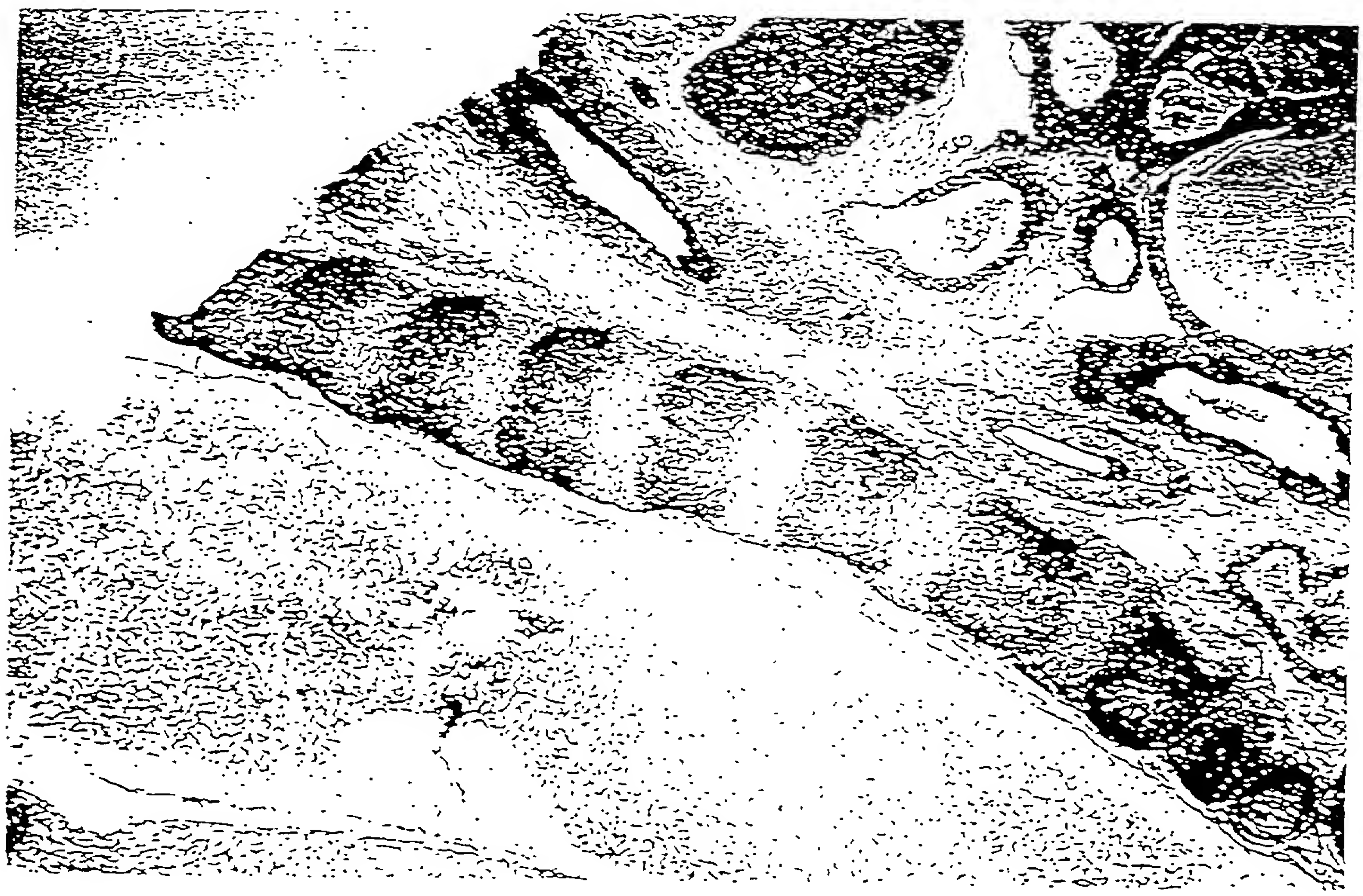


Figure 17A

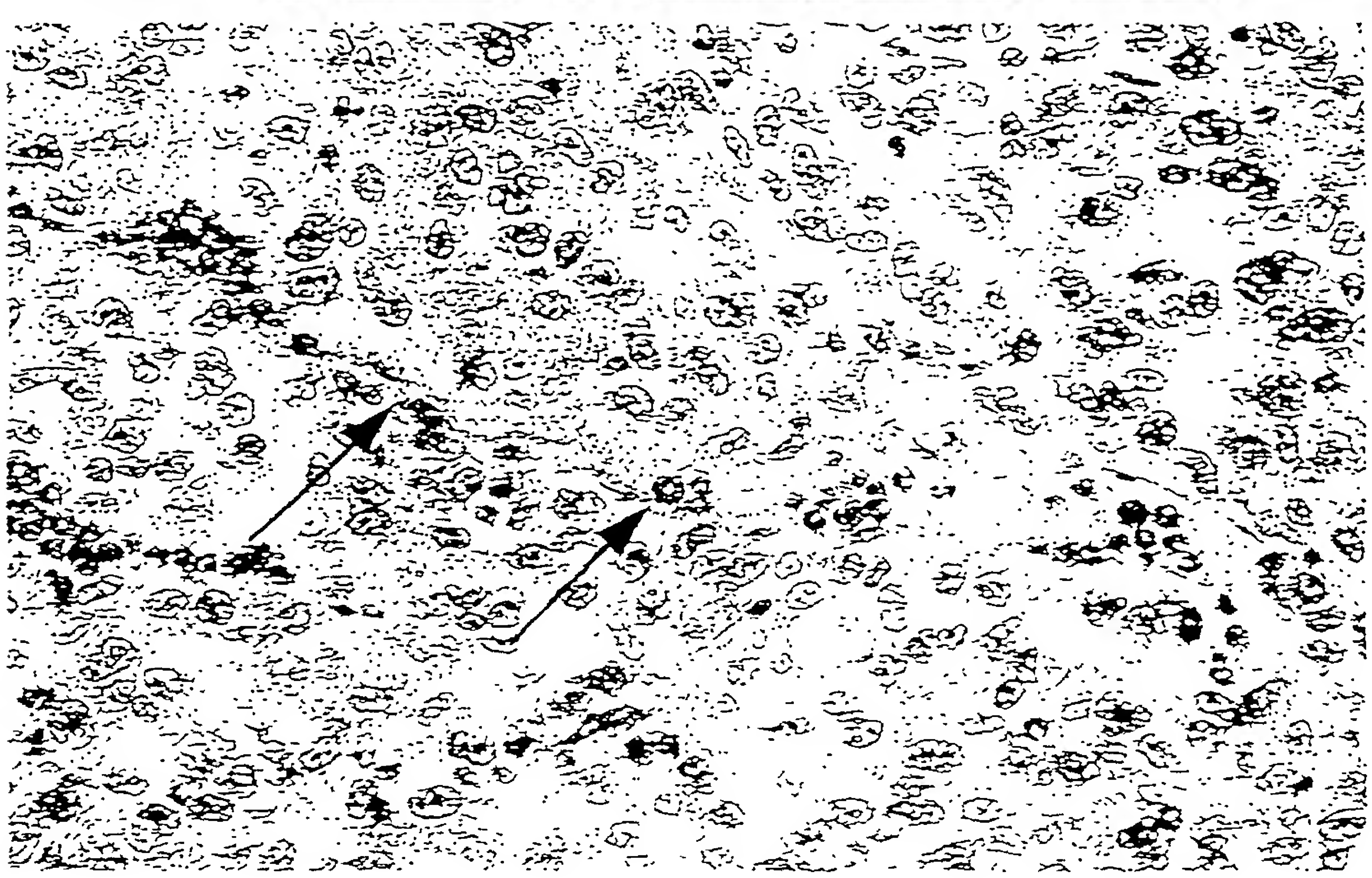
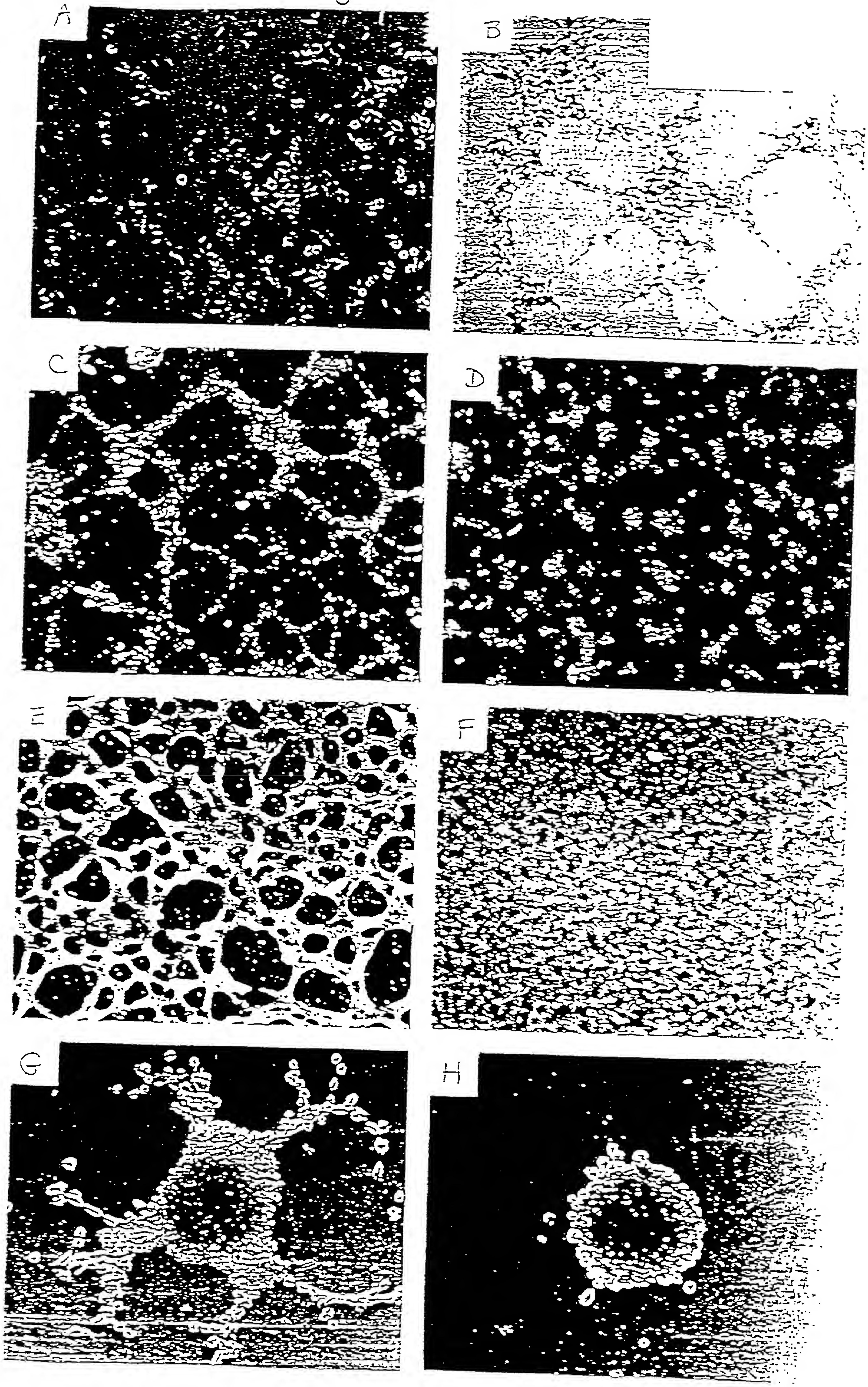
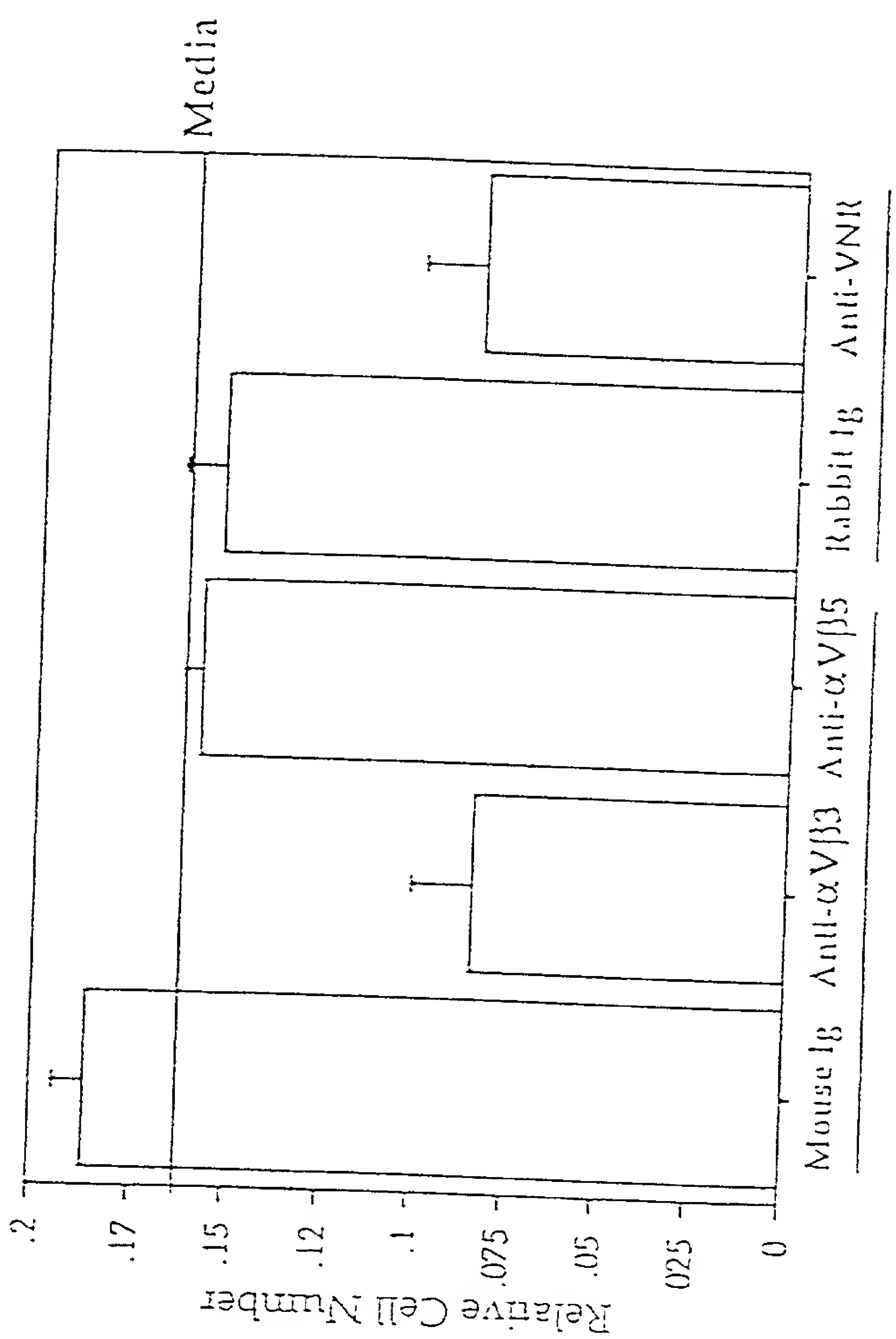


Figure 17B

8907-034 (sheet 29 of 32)
Figure 18A - 18H



8907-034 (Sheet 30 of 32)
Figure 19



8907-034 (Sheet 31 of 32)
Figure 20

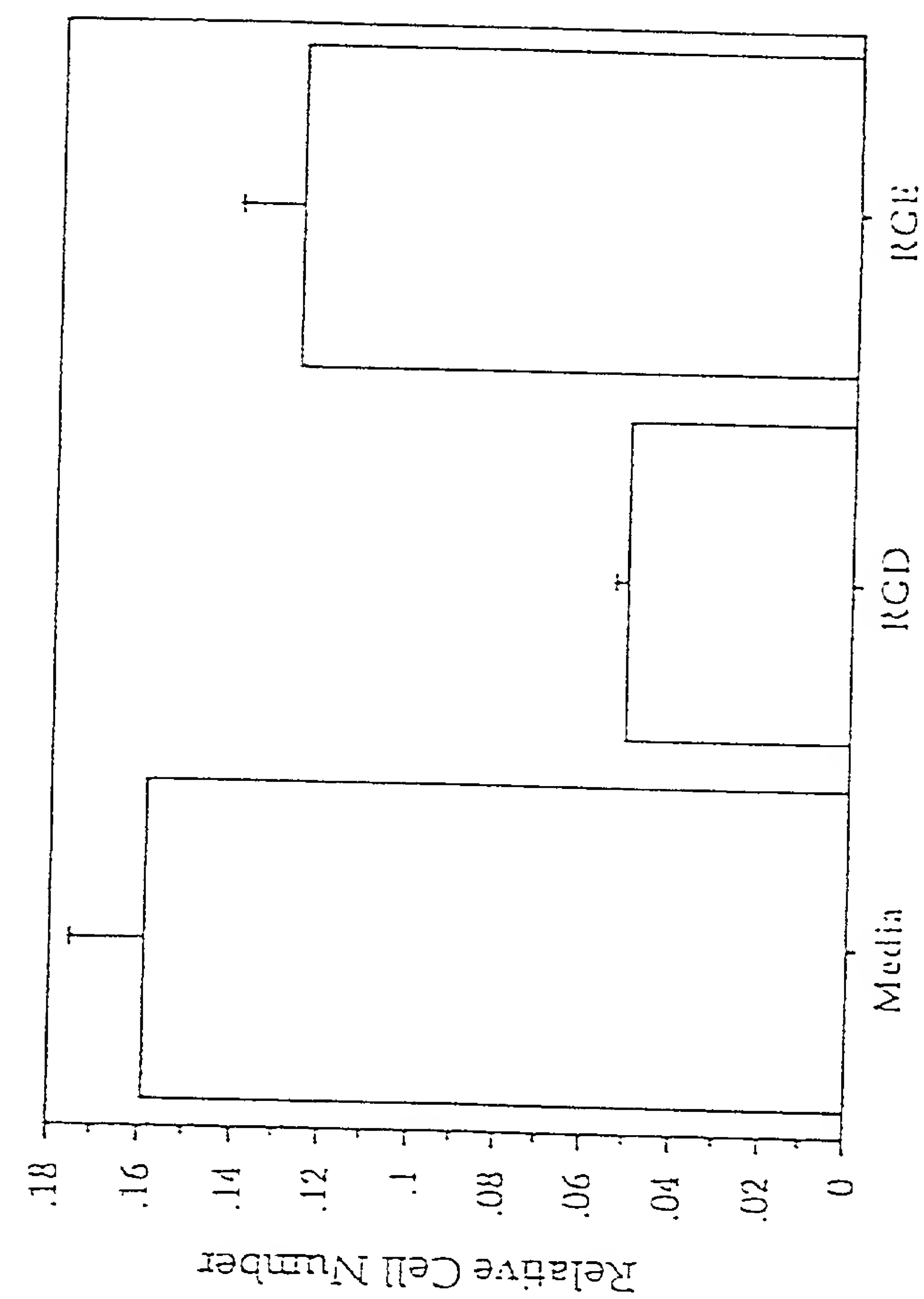
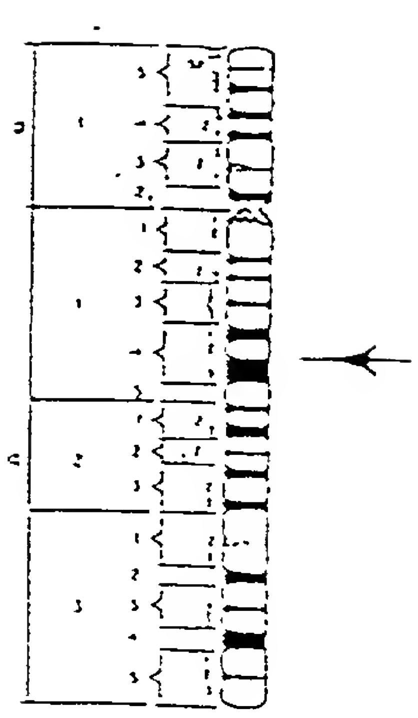


Figure 21A

5

Figure 21B



5

DECLARATION
AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below at 201 et seq. underneath my name.

I believe I am the original, first and sole inventor if only one name is listed at 201 below, or an original, first and joint inventor if plural names are listed at 201 et seq. below, of the subject matter which is claimed and for which a patent is sought on the invention entitled

DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

and for which a patent application:
☐ is attached hereto and includes amendment(s) filed on _______ *(if applicable)*
☒ was filed in the United States on June 5, 1996 as Application Serial No. 08/659,235 *(for declaration not accompanying application)*
with amendment(s) filed on _______________ *(if applicable)*
☐ was filed as PCT international application Serial No. _______________ on _______________ and was amended under PCT Article 19 on _______________ *(if applicable)*

I hereby state that I have reviewed and understand the contents of the above identified application, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED PRIOR TO THE FILING DATE OF THE APPLICATION			
APPLICATION NUMBER	COUNTRY	DATE OF FILING (day, month, year)	PRIORITY CLAIMED
			YES ☐ NO ☐
			YES ☐ NO ☐

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code §112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

APPLICATION SERIAL NO.	FILING DATE	STATUS		
		PATENTED	PENDING	ABANDONED
08/480,229	June 7, 1995		X	

POWER OF ATTORNEY: As a named inventor, I hereby appoint S. Leslie Misrock (Reg. No. 18872), Harry C. Jones, III (Reg. No. 20280), Berj A. Terzian (Reg. No. 20060), Gerald J. Flintoft (Reg. No. 20823), David Weild, III (Reg. No. 21094), Jonathan A. Marshall (Reg. No. 24614), Barry D. Rein (Reg. No. 22411), Stanton T. Lawrence, III (Reg. No. 25736), Isaac Jarkovsky (Reg. No. 22713), Joseph V. Colaianni (Reg. No. 20019), Charles E. McKenney (Reg. No. 22795), Philip T. Shannon (Reg. No. 24278), Francis E. Morris (Reg. No. 24615), Charles E. Miller (Reg. No. 24576), Gidon D. Stern (Reg. No. 27469), John J. Lauter, Jr. (Reg. No. 27814), Brian M. Poissant (Reg. No. 28462), Brian D. Coggio (Reg. No. 27624), Rory J. Radding (Reg. No. 28749), Stephen J. Harbulak (Reg. No. 29166), Donald J. Goodell (Reg. No. 19766), James N. Palik (Reg. No. 25510), Thomas E. Friebel (Reg. No. 29258), Laura A. Coruzzi (Reg. No. 30742), Jennifer Gordon (Reg. No. 30753), Jon R. Stark (Reg. No. 30111), Allan A. Fanucci (Reg. No. 30256), Geraldine F. Baldwin (Reg. No. 31232), Victor N. Balancia (Reg. No. 31231), Albert P. Halluin (Reg. No. 25227), Samuel B. Abrams (Reg. No. 30605), Steven I. Wallach (Reg. No. 35402), Marcia H. Sundeen (Reg. No. 30893), Paul J. Zegger (Reg. No. 33821), Edmond R. Bannon (Reg. No. 32110), Bruce J. Barker (Reg. No. 33291), Adriane M. Antler (Reg. No. 32605), Ann L. Gisolfi (Reg. No. 31956), SaraLynn Mandel (Reg. No 31853), Mark A. Farley (Reg. No. 33170), James G Markey (Reg. No. 31636), and Charles F. Hoyng (Reg. No. 35548), all of Pennie & Edmonds, whose addresses are 1155 Avenue of the Americas, New York, New York 10036, 1667 K Street N.W., Washington, DC 20006 and 2730 Sand Hill Road, Menlo Park, CA 94025, and each of them, my attorneys, to prosecute this application, and to transact all business in the Patent and Trademark Office connected therewith.

SEND CORRESPONDENCE TO: PENNIE & EDMONDS
1155 AVENUE OF THE AMERICAS
NEW YORK, N.Y. 10036-2711

DIRECT TELEPHONE CALLS TO:
PENNIE & EDMONDS DOCKETING
(212) 790-2803

201	FULL NAME OF INVENTOR	LAST NAME Quertermous	FIRST NAME Thomas	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY Nashville	STATE OR FOREIGN COUNTRY Tennessee	COUNTRY OF CITIZENSHIP U.S.A.	
	POST OFFICE ADDRESS	STREET 3417 Valley Brook Road	CITY Nashville	STATE OR COUNTRY Tennessee	ZIP CODE 37215
202	FULL NAME OF INVENTOR	LAST NAME Hogan	FIRST NAME Brigid	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY Brentwood	STATE OR FOREIGN COUNTRY Tennessee	COUNTRY OF CITIZENSHIP United Kingdom	
	POST OFFICE ADDRESS	STREET 1303 Robert E. Lee Lane	CITY Brentwood	STATE OR COUNTRY Tennessee	ZIP CODE 37027
203	FULL NAME OF INVENTOR	LAST NAME Snodgrass	FIRST NAME H.	MIDDLE NAME Ralph	
	RESIDENCE & CITIZENSHIP	CITY Powell	STATE OR FOREIGN COUNTRY Ohio	COUNTRY OF CITIZENSHIP U.S.A.	
	POST OFFICE ADDRESS	STREET 650 Retreat Lane	CITY Powell	STATE OR COUNTRY Ohio	ZIP CODE 43065
204	FULL NAME OF INVENTOR	LAST NAME Zupancic	FIRST NAME Thomas	MIDDLE NAME Joel	
	RESIDENCE & CITIZENSHIP	CITY Worthington	STATE OR FOREIGN COUNTRY Ohio	COUNTRY OF CITIZENSHIP U.S.A.	
	POST OFFICE ADDRESS	STREET 501 Park Boulevard	CITY Worthington	STATE OR COUNTRY Ohio	ZIP CODE 43085
205	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP	
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY	ZIP CODE
206	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP	
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY	ZIP CODE

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

SIGNATURE OF INVENTOR 201 Thomas Quertermous	SIGNATURE OF INVENTOR 202 Brigid Hogan	SIGNATURE OF INVENTOR 203 H. Ralph Snodgrass H. Ralph Snodgrass
DATE	DATE	DATE 9/4/96
SIGNATURE OF INVENTOR 204 Tom Zupancic Thomas Joel Zupancic	SIGNATURE OF INVENTOR 205	SIGNATURE OF INVENTOR 206
DATE 9/4/96	DATE	DATE

PEMP-61557.1

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below at 201 et seq. underneath my name.

I believe I am the original, first and sole inventor if only one name is listed at 201 below, or an original, first and joint inventor if plural names are listed at 201 et seq. below, of the subject matter which is claimed and for which a patent is sought on the invention entitled

DEVELOPMENTALLY-REGULATED ENDOTHELIAL CELL LOCUS-1

and for which a patent application:
☐ is attached hereto and includes amendment(s) filed on _______ *(if applicable)*
☒ was filed in the United States on June 5, 1996 as Application Serial No. 08/659,235 *(for declaration not accompanying application)*
with amendment(s) filed on ________________ *(if applicable)*
☐ was filed as PCT international application Serial No. _______________ on _______________ and was amended under PCT Article 19 on _______________ *(if applicable)*

I hereby state that I have reviewed and understand the contents of the above identified application, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED PRIOR TO THE FILING DATE OF THE APPLICATION				
APPLICATION NUMBER	COUNTRY	DATE OF FILING (day, month, year)	PRIORITY CLAIMED	
			YES ☐	NO ☐
			YES ☐	NO ☐

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code §112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

APPLICATION SERIAL NO.	FILING DATE	STATUS		
		PATENTED	PENDING	ABANDONED
08/480,229	June 7, 1995		X	

POWER OF ATTORNEY: As a named inventor, I hereby appoint S. Leslie Misrock (Reg. No. 18872), Harry C. Jones, III (Reg. No. 20280), Berj A. Terzian (Reg. No. 20060), Gerald J. Flintoft (Reg. No. 20823), David Weild, III (Reg. No. 21094), Jonathan A. Marshall (Reg. No. 24614), Barry D. Rein (Reg. No. 22411), Stanton T. Lawrence, III (Reg. No. 25736), Isaac Jarkovsky (Reg. No. 22713), Joseph V. Colaianni (Reg. No. 20019), Charles E. McKenney (Reg. No. 22795), Philip T. Shannon (Reg. No. 24278), Francis E. Morris (Reg. No. 24615), Charles E. Miller (Reg. No. 24576), Gidon D. Stern (Reg. No. 27469), John J. Lauter, Jr. (Reg. No. 27814), Brian M. Poissant (Reg. No. 28462), Brian D. Coggio (Reg. No. 27624), Rory J. Radding (Reg. No. 28749), Stephen J. Harbulak (Reg. No. 29166), Donald J. Goodell (Reg. No. 19766), James N. Palik (Reg. No. 25510), Thomas E. Friebel (Reg. No. 29258), Laura A. Coruzzi (Reg. No. 30742), Jennifer Gordon (Reg. No. 30753), Jon R. Stark (Reg. No. 30111), Allan A. Fanucci (Reg. No. 30256), Geraldine F. Baldwin (Reg. No. 31232), Victor N. Balancia (Reg. No. 31231), Albert P. Halluin (Reg. No. 25227), Samuel B. Abrams (Reg. No. 30605), Steven I. Wallach (Reg. No. 35402), Marcia H. Sundeen (Reg. No. 30893), Paul J. Zegger (Reg. No. 33821), Edmond R. Bannon (Reg. No. 32110), Bruce J. Barker (Reg. No. 33291), Adriane M. Antler (Reg. No. 32605), Ann L. Gisolfi (Reg. No. 31956), SaraLynn Mandel (Reg. No. 31853), Mark A. Farley (Reg. No. 33170), James G. Markey (Reg. No. 31636), and Charles F. Hoyng (Reg. No. 35548), all of Pennie & Edmonds, whose addresses are 1155 Avenue of the Americas, New York, New York 10036, 1667 K Street N.W., Washington, DC 20006 and 2730 Sand Hill Road, Menlo Park, CA 94025, and each of them, my attorneys, to prosecute this application, and to transact all business in the Patent and Trademark Office connected therewith.

SEND CORRESPONDENCE TO: PENNIE & EDMONDS
1155 AVENUE OF THE AMERICAS
NEW YORK, N.Y. 10036-2711

DIRECT TELEPHONE CALLS TO:
PENNIE & EDMONDS DOCKETING
(212) 790-2803

201	FULL NAME OF INVENTOR	LAST NAME: Quertermous	FIRST NAME: Thomas	MIDDLE NAME:	
	RESIDENCE & CITIZENSHIP	CITY: Nashville	STATE OR FOREIGN COUNTRY: Tennessee	COUNTRY OF CITIZENSHIP: U.S.A.	
	POST OFFICE ADDRESS	STREET: 3417 Valley Brook Road	CITY: Nashville	STATE OR COUNTRY: Tennessee	ZIP CODE: 37215
202	FULL NAME OF INVENTOR	LAST NAME: Hogan	FIRST NAME: Brigid	MIDDLE NAME:	
	RESIDENCE & CITIZENSHIP	CITY: Brentwood	STATE OR FOREIGN COUNTRY: Tennessee	COUNTRY OF CITIZENSHIP: United Kingdom	
	POST OFFICE ADDRESS	STREET: 1303 Robert E. Lee Lane	CITY: Brentwood	STATE OR COUNTRY: Tennessee	ZIP CODE: 37027
203	FULL NAME OF INVENTOR	LAST NAME: Snodgrass	FIRST NAME: H.	MIDDLE NAME: Ralph	
	RESIDENCE & CITIZENSHIP	CITY: Powell	STATE OR FOREIGN COUNTRY: Ohio	COUNTRY OF CITIZENSHIP: U.S.A.	
	POST OFFICE ADDRESS	STREET: 650 Retreat Lane	CITY: Powell	STATE OR COUNTRY: Ohio	ZIP CODE: 43065
204	FULL NAME OF INVENTOR	LAST NAME: Zupancic	FIRST NAME: Thomas	MIDDLE NAME: Joel	
	RESIDENCE & CITIZENSHIP	CITY: Worthington	STATE OR FOREIGN COUNTRY: Ohio	COUNTRY OF CITIZENSHIP: U.S.A.	
	POST OFFICE ADDRESS	STREET: 501 Park Boulevard	CITY: Worthington	STATE OR COUNTRY: Ohio	ZIP CODE: 43085
205	FULL NAME OF INVENTOR	LAST NAME:	FIRST NAME:	MIDDLE NAME:	
	RESIDENCE & CITIZENSHIP	CITY:	STATE OR FOREIGN COUNTRY:	COUNTRY OF CITIZENSHIP:	
	POST OFFICE ADDRESS	STREET:	CITY:	STATE OR COUNTRY:	ZIP CODE:
206	FULL NAME OF INVENTOR	LAST NAME:	FIRST NAME:	MIDDLE NAME:	
	RESIDENCE & CITIZENSHIP	CITY:	STATE OR FOREIGN COUNTRY:	COUNTRY OF CITIZENSHIP:	
	POST OFFICE ADDRESS	STREET:	CITY:	STATE OR COUNTRY:	ZIP CODE:

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

SIGNATURE OF INVENTOR 201: Thomas Quertermous	SIGNATURE OF INVENTOR 202: B Hogan Brigid Hogan	SIGNATURE OF INVENTOR 203: H. Ralph Snodgrass
DATE: 9-6-96	DATE: 9-26-96	DATE:
SIGNATURE OF INVENTOR 204: Thomas Joel Zupancic	SIGNATURE OF INVENTOR 205:	SIGNATURE OF INVENTOR 206:
DATE:	DATE:	DATE: